

FIGURE 1A

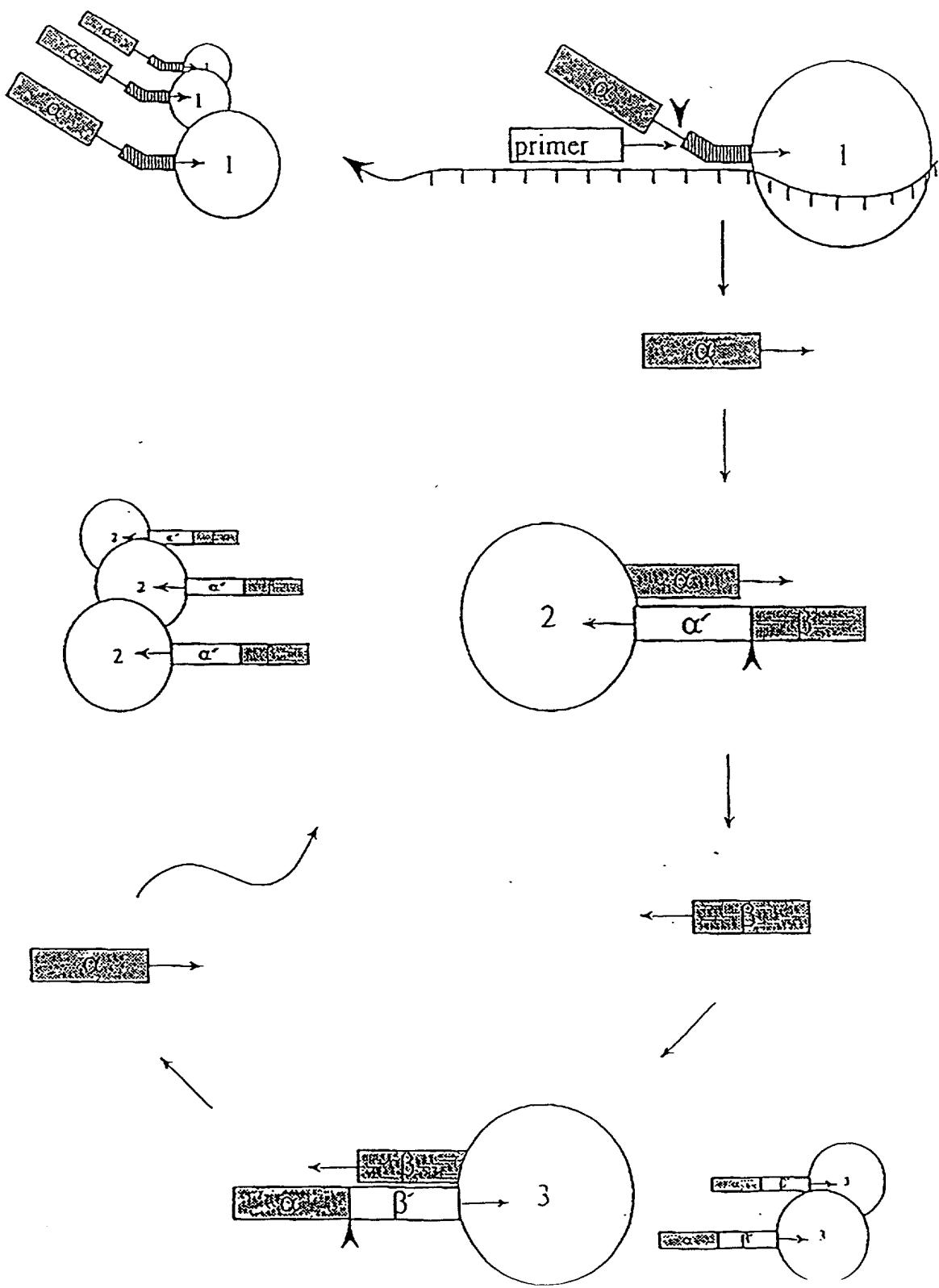
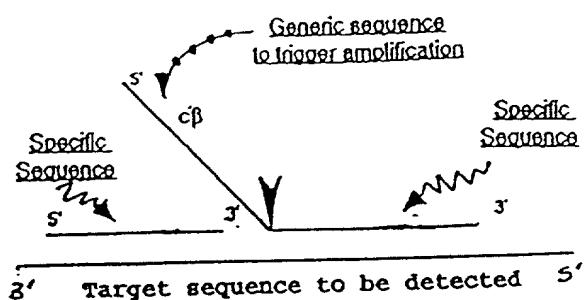


FIGURE 1 B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION

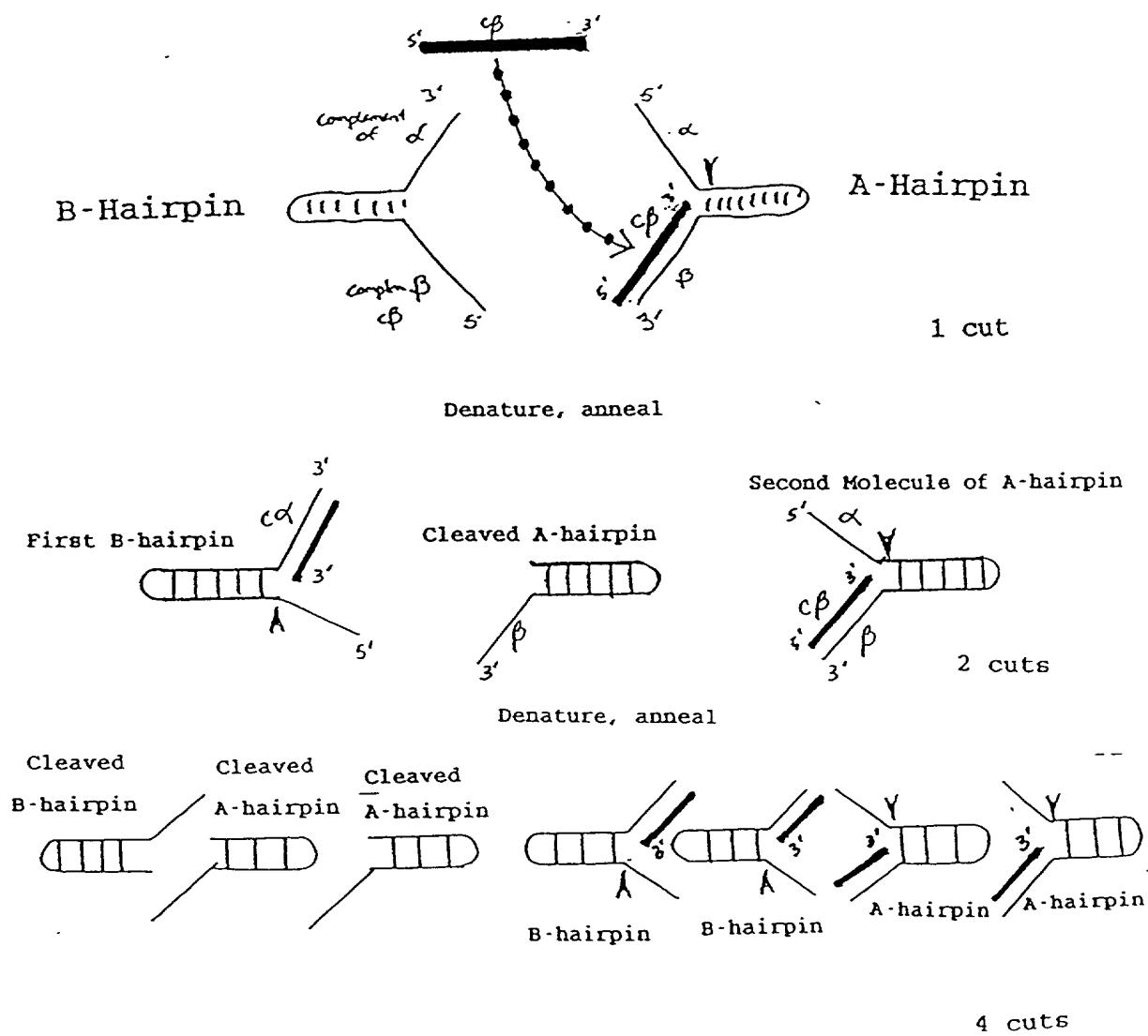


FIGURE 2

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	CCCCCTGGAGGTGGACGTGGGATGGGGAGCTGGCTCTGGCTAAGGAGTAG	2499
DNAPTAQ (SEQ ID NO:1)A.....	2496
DNAPTR (SEQ ID NO:2)CC.....	2505
DNAPTH (SEQ ID NO:3)T.....	

FIGURE 3

MAJORITY (SEQ ID NO:8)	MIX A M L P L F E P K G R V L L V D O G H H L A Y R T F F A L K G L T T S R G E P V Q A V Y G F A K S L L K A L K E D G . D A V X V V F D A R	69
TAQ PRO (SEQ ID NO:4)	R G	68
TR PRO (SEQ ID NO:5)	70
TH PRO (SEQ ID NO:6)	E	
MAJORITY	A P S F R H E A Y E A Y K A G R A P T P E D F P R O L A L I K E L V D O L I G L X R L E V P G Y E A D D V V A T L A K K A E K E G Y E V R I L	
TAQ PRO	H	
TR PRO	G G	139
TH PRO	V	
MAJORITY	A P S F R H E A Y E A Y K A G R A P T P E D F P R O L A L I K E L V D O L I G L X R L E V P G Y E A D D V V A T L A K K A E K E G Y E V R I L	
TAQ PRO	H	
TR PRO	G G	139
TH PRO	V	
MAJORITY	T A D R O L Y Y O L I S D R I A V L H P E G Y L I T P A W L W E K Y G L R P E Q W W D Y R A L X G D P S D N L P G V K G I G E K T A X K L L X	
TAQ PRO	K	
TR PRO	E	
TH PRO	V	
MAJORITY	T A D R O L Y Y O L I S D R I A V L H P E G Y L I T P A W L W E K Y G L R P E Q W W D Y R A L X G D P S D N L P G V K G I G E K T A X K L L X	
TAQ PRO	H	
TR PRO	I	
TH PRO	E	
MAJORITY	F W G S L E N L L K N H L D R V K P . X X R E K I X A H M E D I X L S X X L S X V R T D L P L E V D F A X R R E P D E G L R A F L E R L E F	
TAQ PRO	A	
TR PRO	A I	
TH PRO	S L	
MAJORITY	A	
TAQ PRO	L	
TR PRO	D	
TH PRO	K	
MAJORITY	K	
TAQ PRO	W D	
TR PRO	A K	
TH PRO	A	
MAJORITY	G R	
TAQ PRO	G	
TR PRO	G	
TH PRO	G	
MAJORITY	T	
TAQ PRO	N L	
TR PRO	N L	
TH PRO	N L	
MAJORITY	G R	
TAQ PRO	G R	
TR PRO	G R	
TH PRO	G R	
MAJORITY	N L	
TAQ PRO	N L	
TR PRO	N L	
TH PRO	N L	
MAJORITY	R	
TAQ PRO	R	
TR PRO	R	
TH PRO	R	
MAJORITY	K	
TAQ PRO	K	
TR PRO	K	
TH PRO	K	
MAJORITY	P E	
TAQ PRO	P E	
TR PRO	P E	
TH PRO	P E	
MAJORITY	Y K A	
TAQ PRO	Y K A	
TR PRO	Y K A	
TH PRO	Y K A	
MAJORITY	A	
TAQ PRO	A	
TR PRO	A	
TH PRO	A	
MAJORITY	G	
TAQ PRO	G	
TR PRO	G	
TH PRO	G	
MAJORITY	G	
TAQ PRO	G	
TR PRO	G	
TH PRO	G	
MAJORITY	S F	
TAQ PRO	L	
TR PRO	S F	
TH PRO	A P	
MAJORITY	K	
TAQ PRO	C D	
TR PRO	C D	
TH PRO	C D	
MAJORITY	K	
TAQ PRO	A	
TR PRO	A	
TH PRO	A	

FIGURE 3 (cont'd)

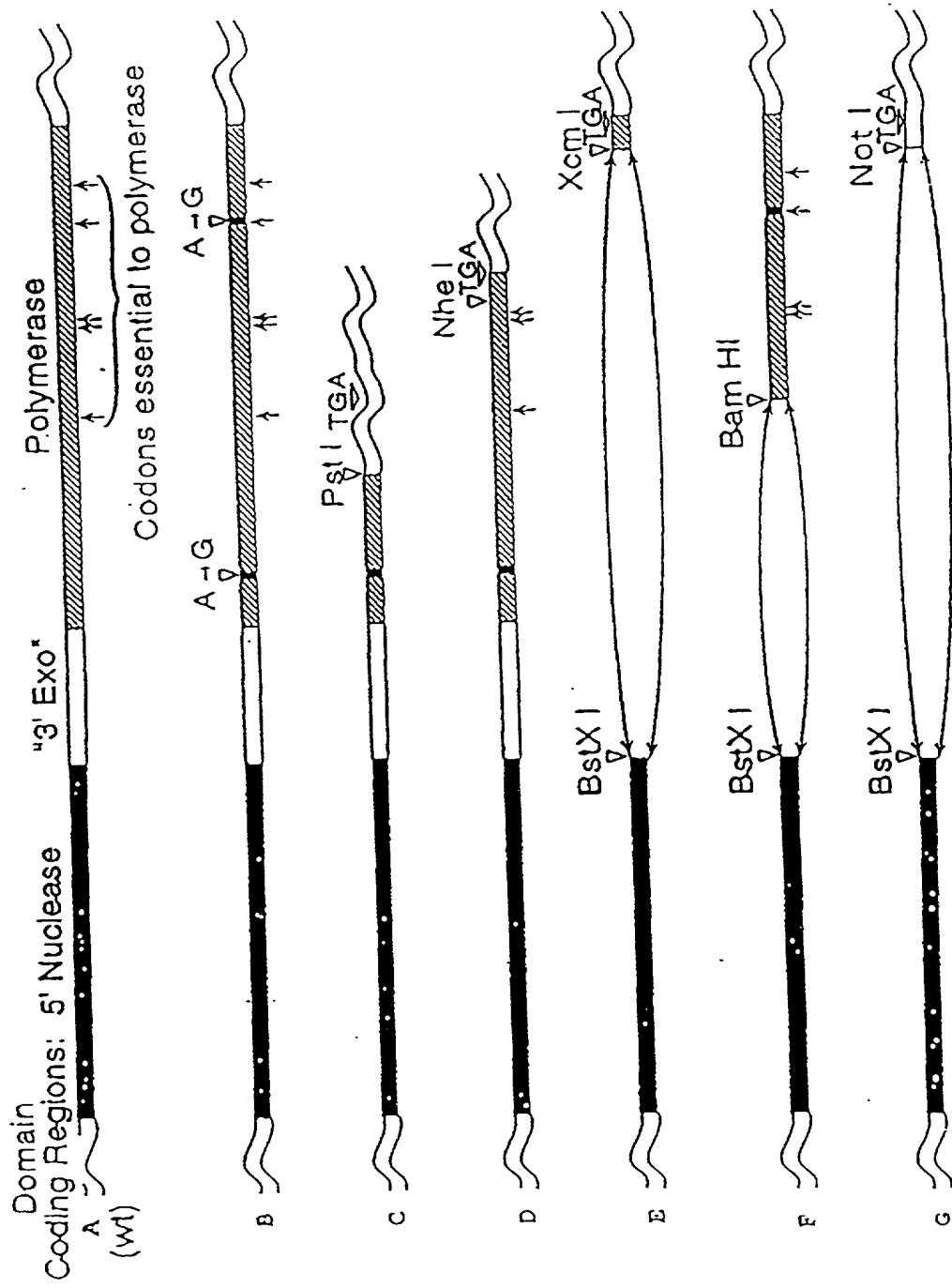
FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8) SFPKVRAWI EKTLE FGRRGYVETLFGRRGYVETLNARVKSUREAAERMAFNMPVQGTAAADLMKLAHVKL
TAQ PRO (SEQ ID NO:4) E.....
TR PRO (SEQ ID NO:5) Y.....G.....
TH PRO (SEQ ID NO:6) K.....

MAJORITY FPRIXEMGARMILQVHDELVLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX
TAQ PRO E.....A.....R.....
TR PRO Q.....L.....D.....R.....W.....Q.....
TH PRO R.....L.....A.....KA.....E.....QA.....A.....KA.....M.....
833
831
835
G

T T G C T T C T G G T G G T G G T G

FIGURE 4



T G G T G G C G A T G G T G G C G

FIGURE 5

Genes for Wild-Type and Pol(-) DNAPTH

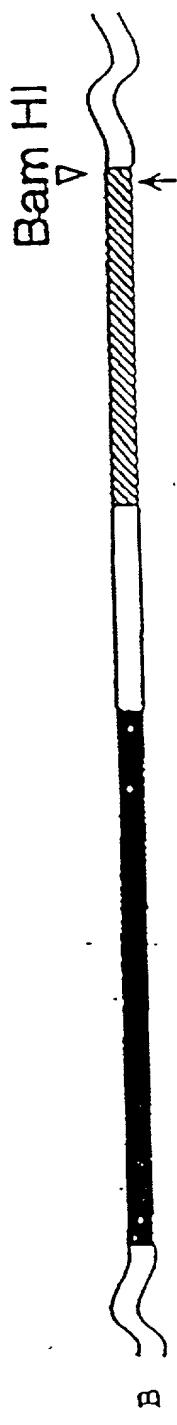
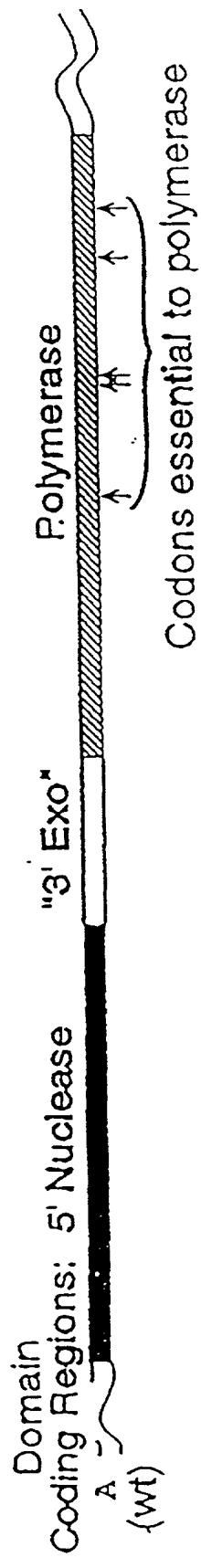


FIGURE 6

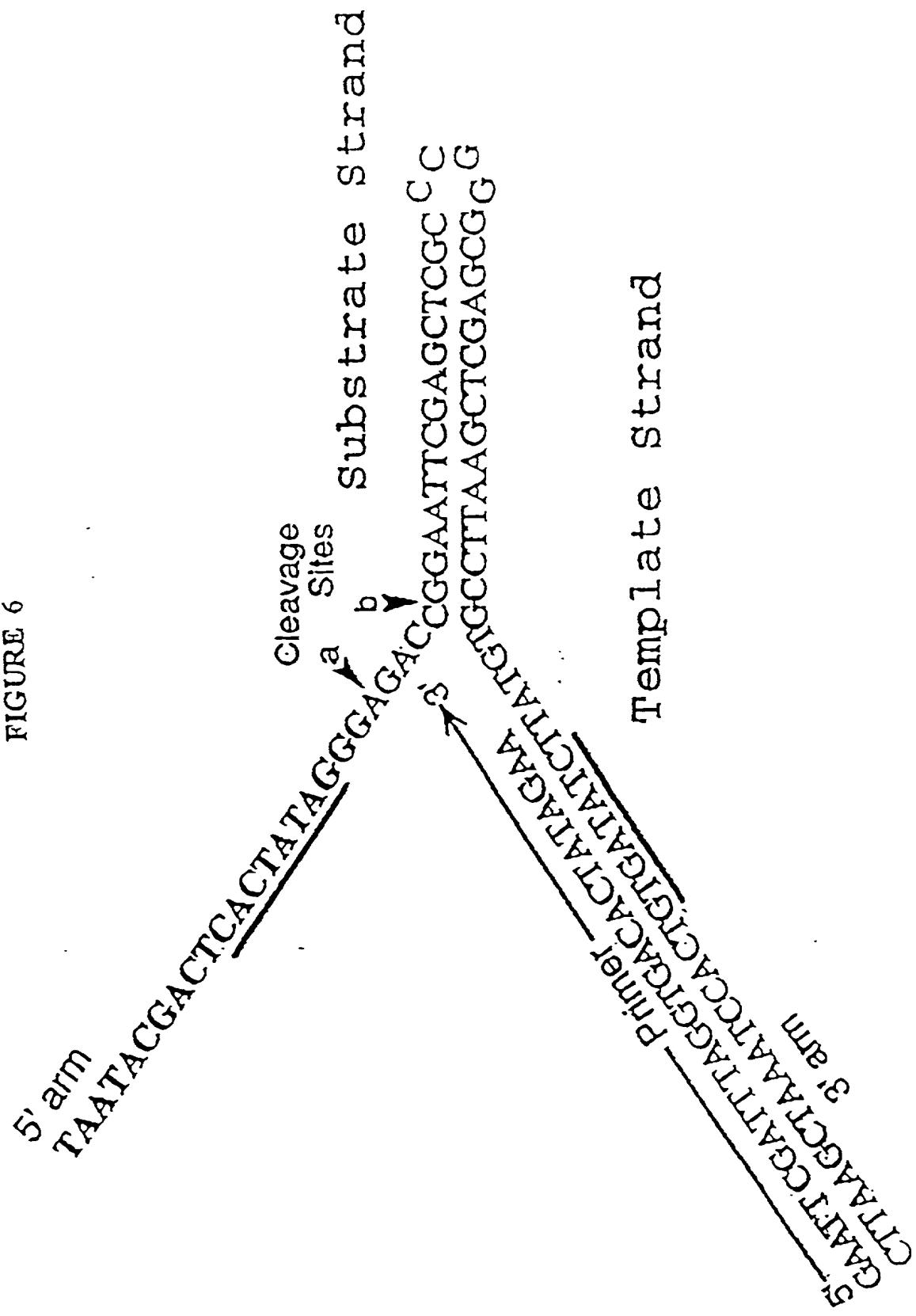


FIGURE 7



(X)

FIGURE 8

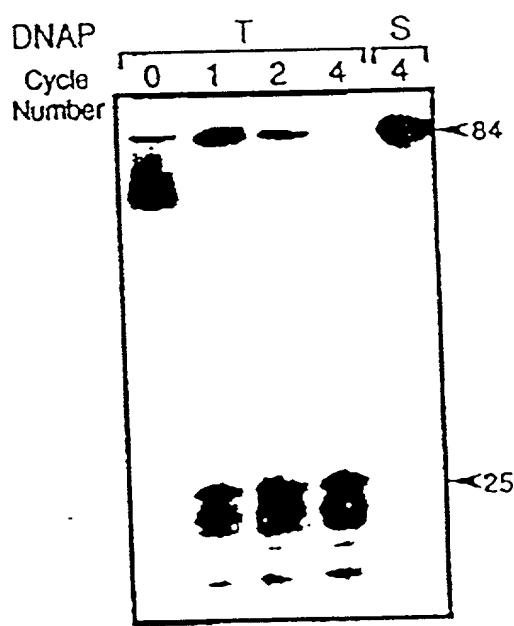


FIGURE 9

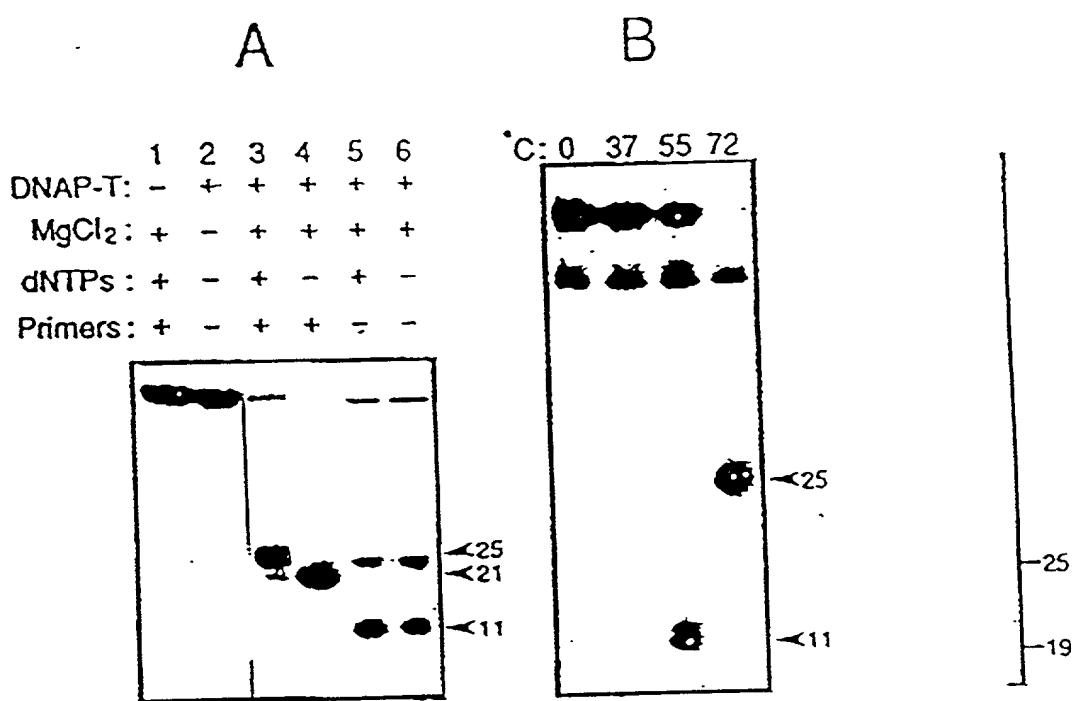


FIGURE 10

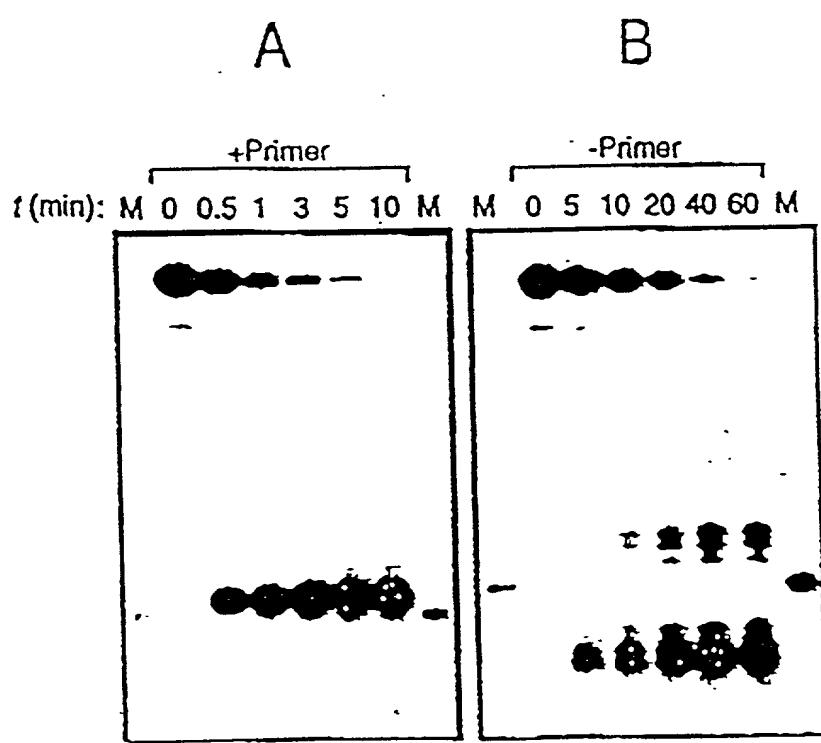
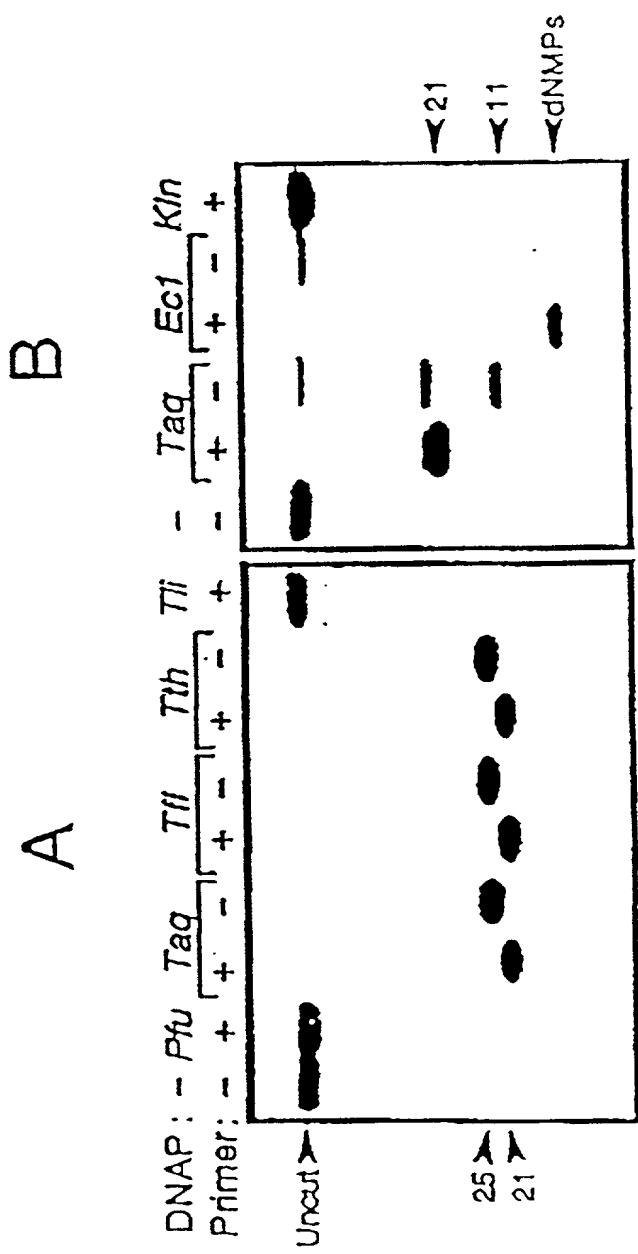
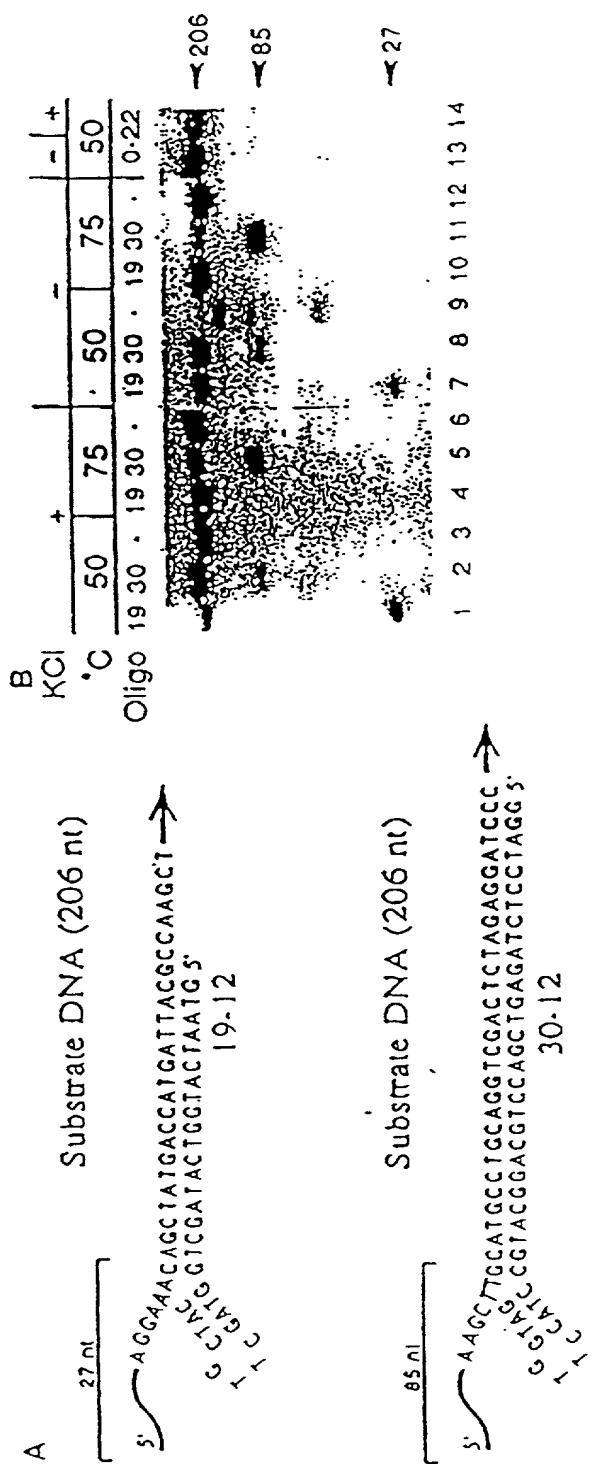


FIGURE 11



21

FIGURE 12



T G G G G G G G G G G G G G G

FIGURE 13

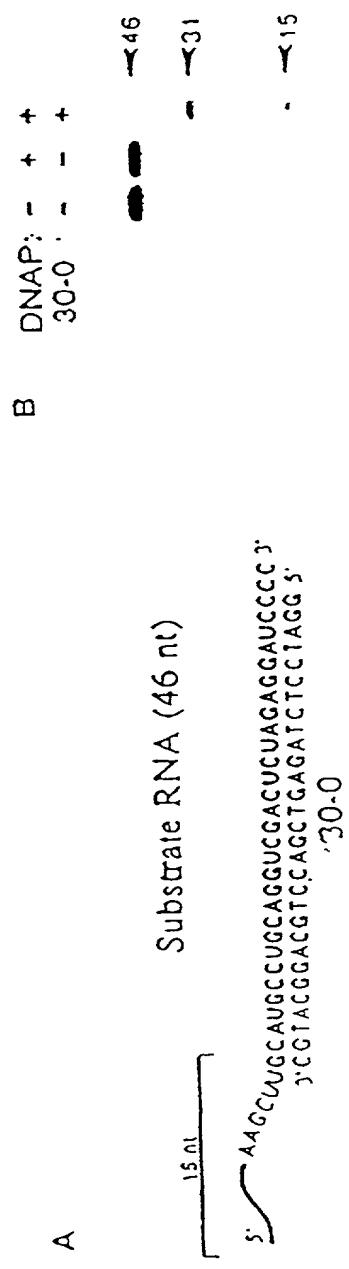
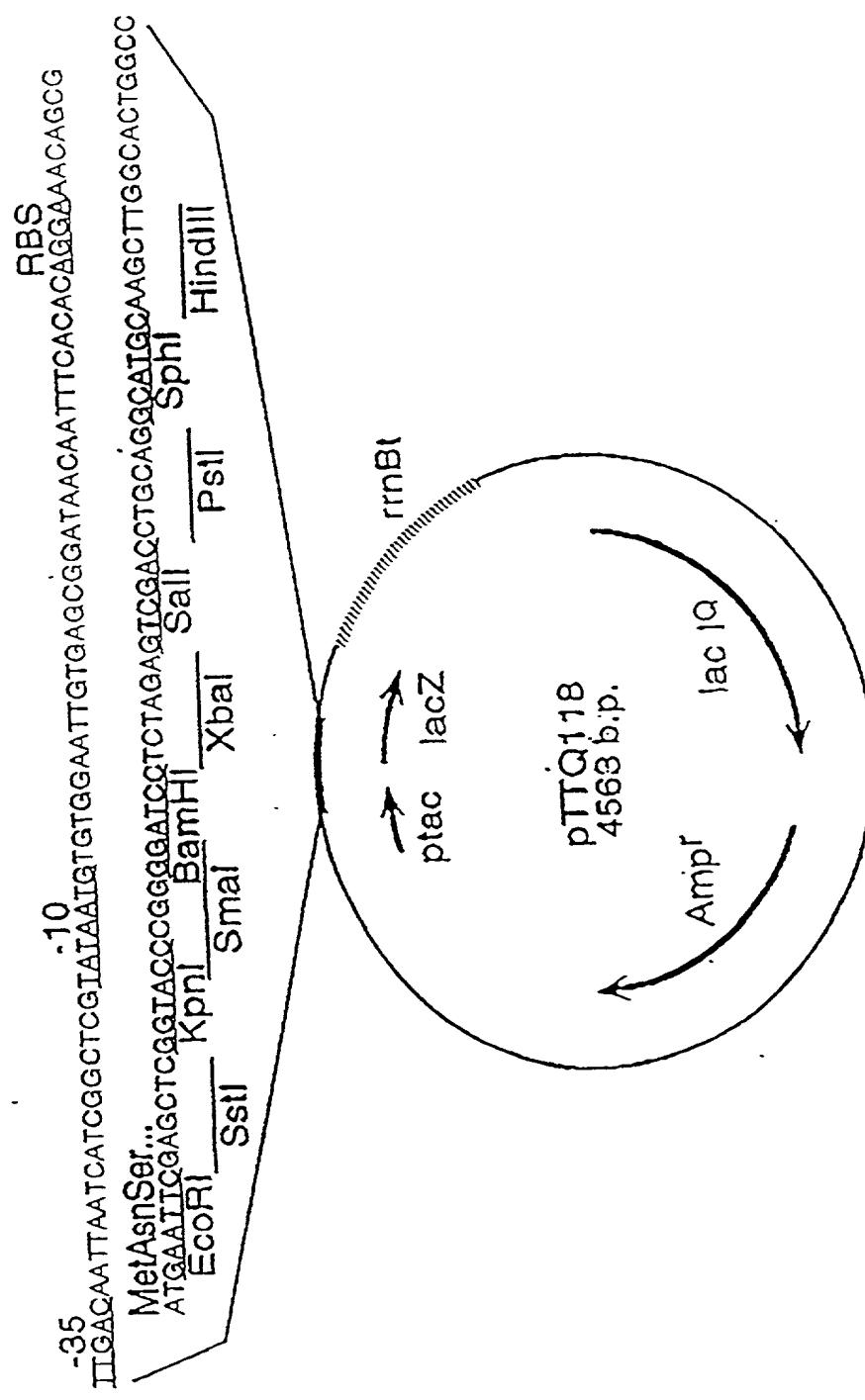


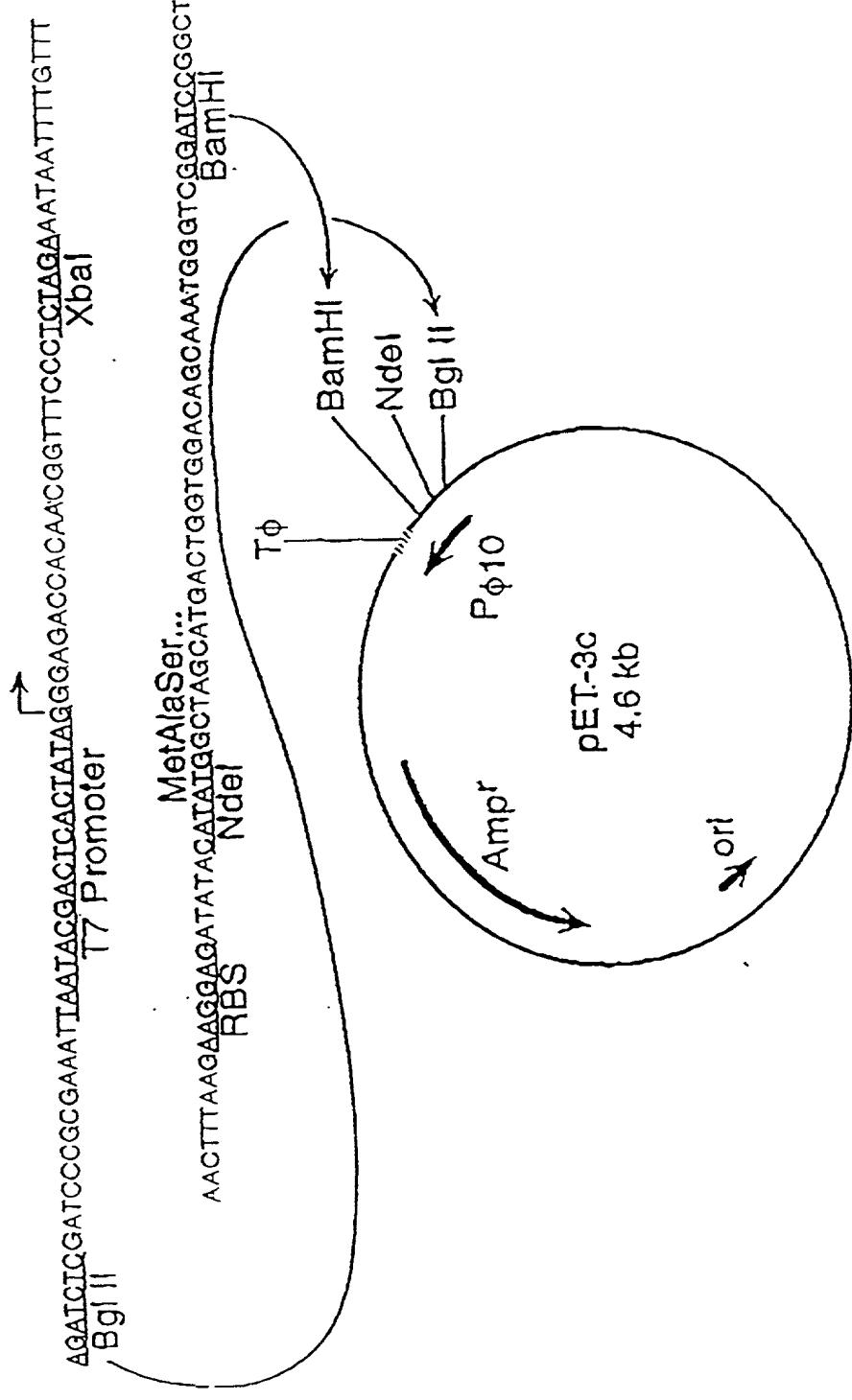
FIGURE 14



RBS: Ribosome binding site
 pTAC: Synthetic tac promoter
 lacI^r: Lac repressor gene

lacZ: Beta-galactosidase alpha fragment
 rrnB^t: E. coli rrnB transcription terminator

FIGURE 15



$p_{\phi 10}$: Bacteriophage T7 $\phi 10$ promoter

$\text{T}\phi$: T7 ϕ Terminator

RBS: Ribosome binding site

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FIGURE 16

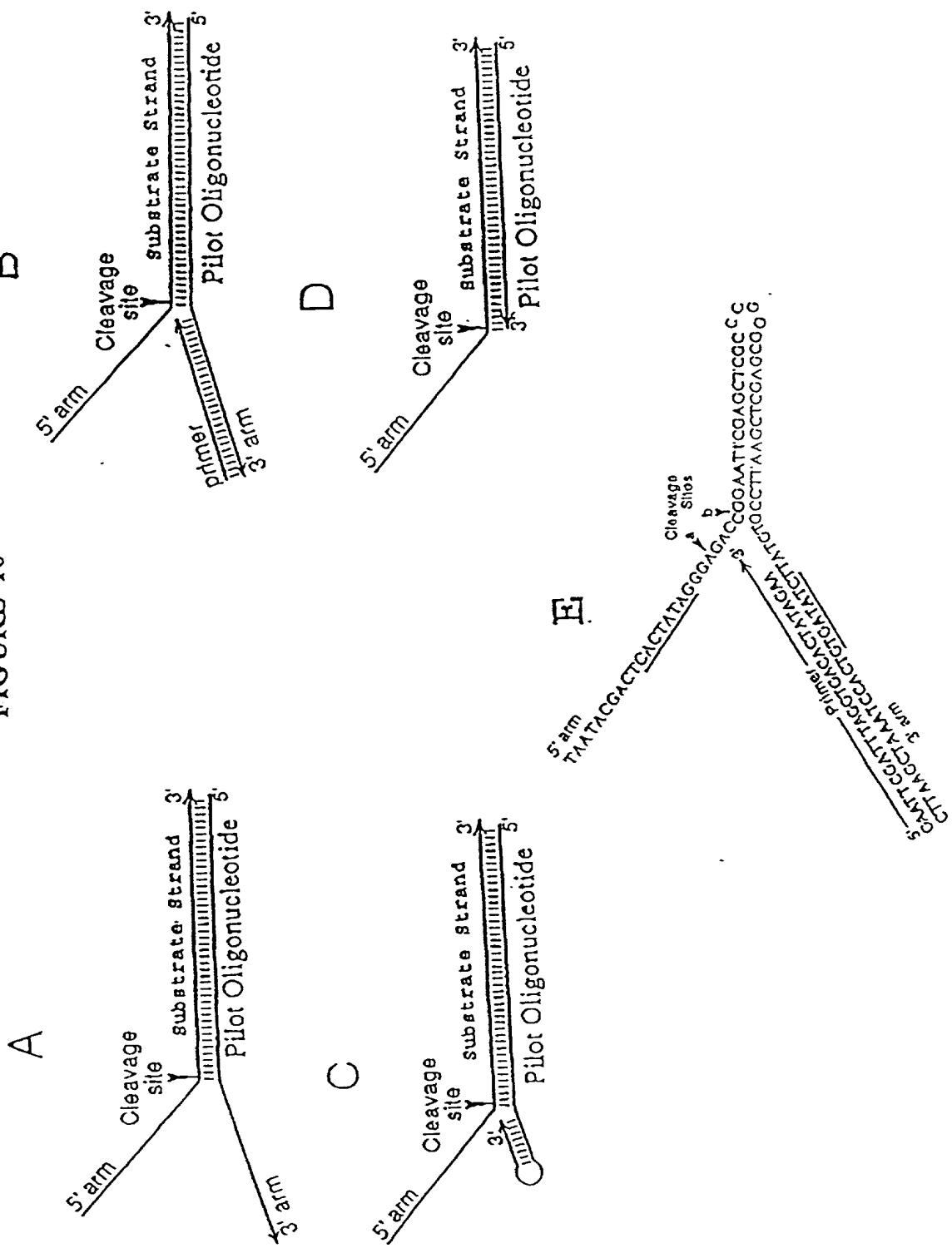


FIGURE 17

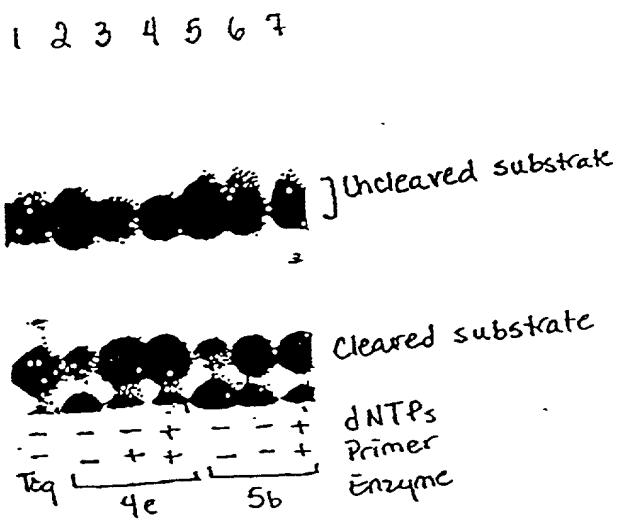


FIGURE 18

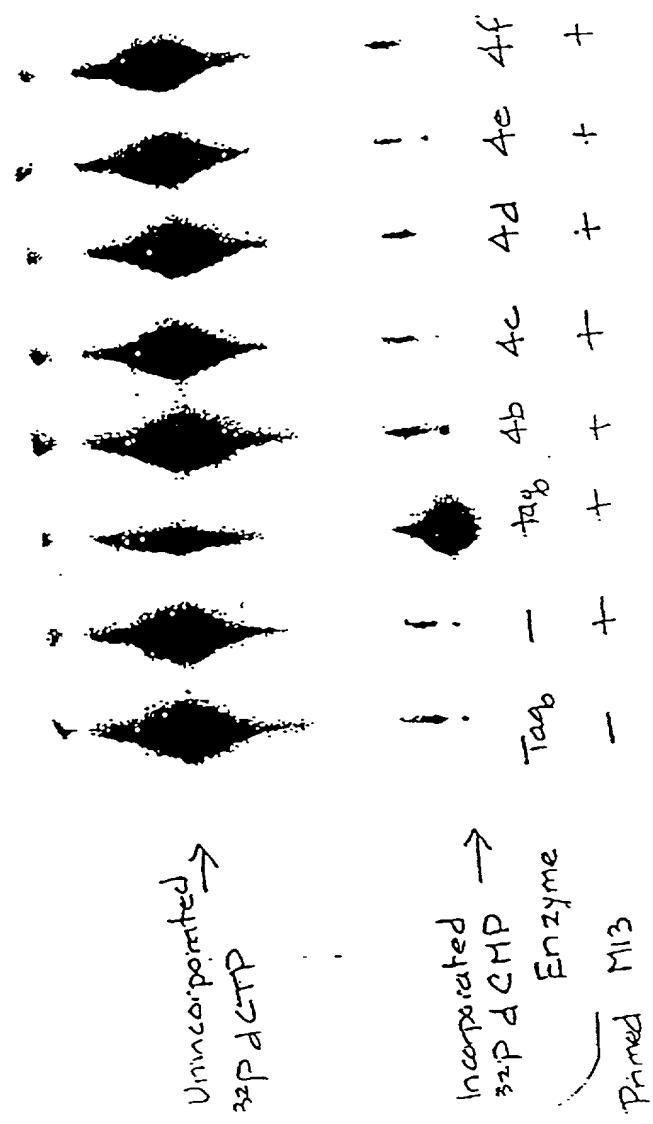
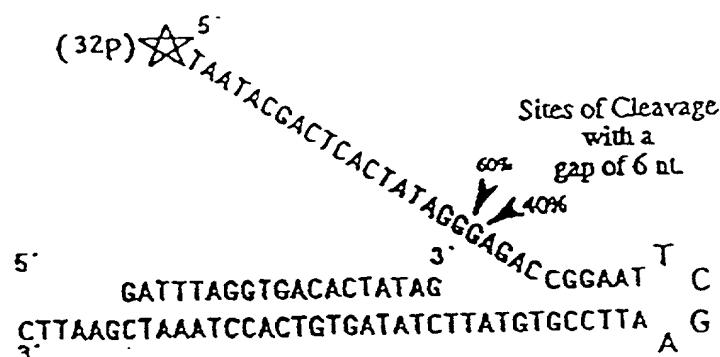


FIGURE 19

A



B

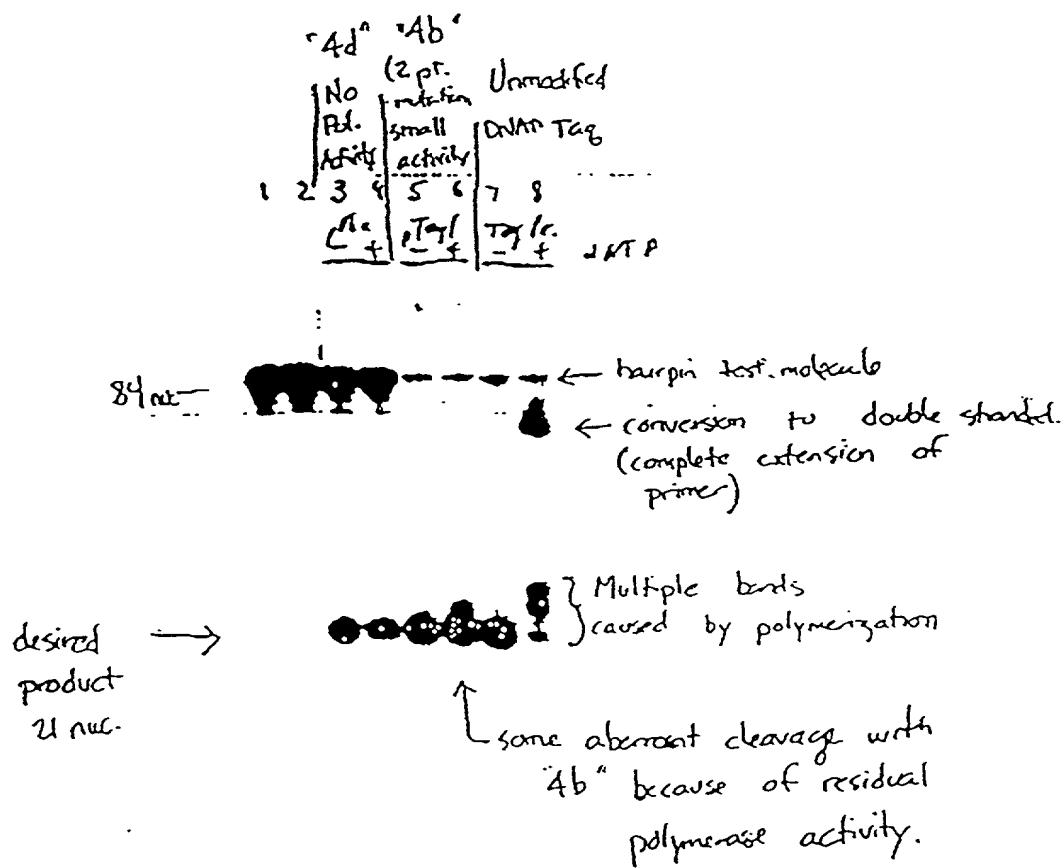
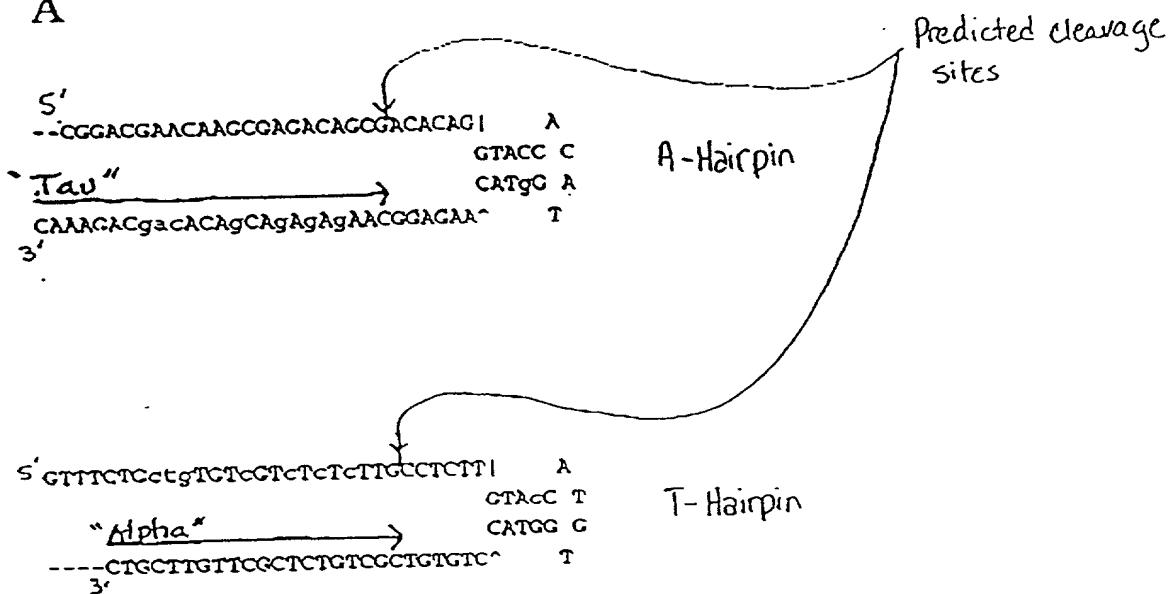


FIGURE 20

A

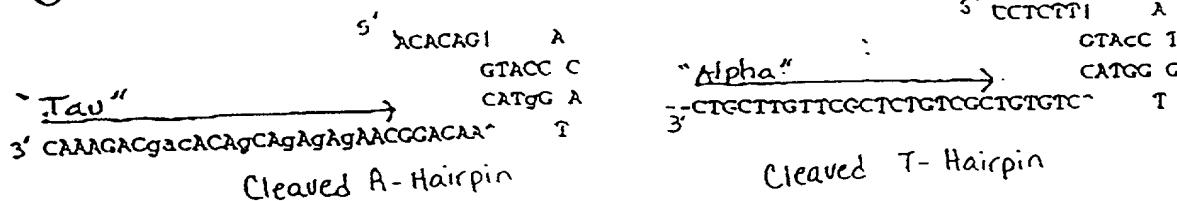


B

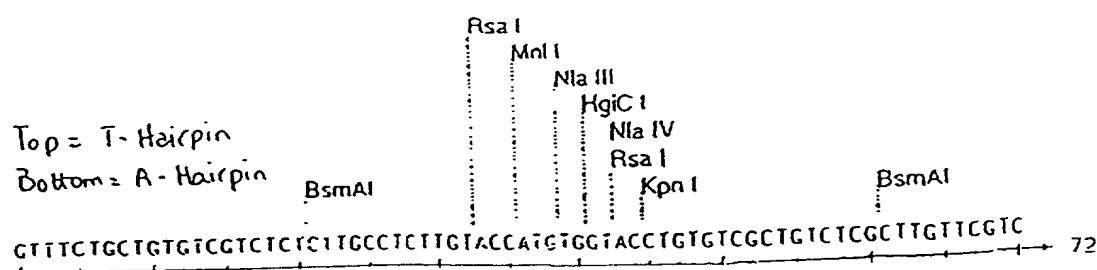
Sequence of alpha primer:

5' GAC GAA CAA CCC AGA AGA CAG CG 3'

C



D



in the same way as the other two, and in fact it is the most difficult of all.

FIGURE 21

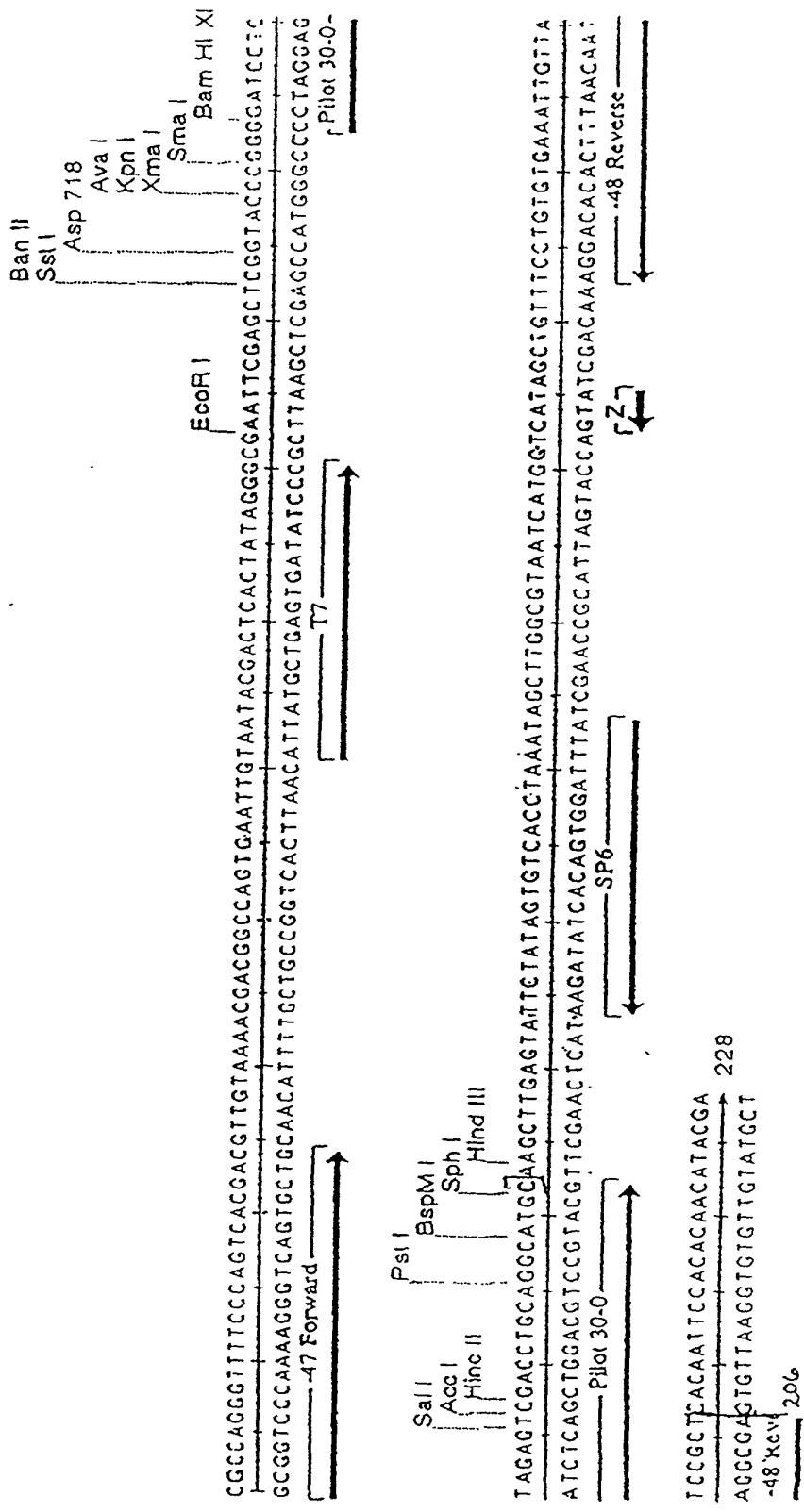


FIGURE 22A

Target Nucleic Acid 206 nt

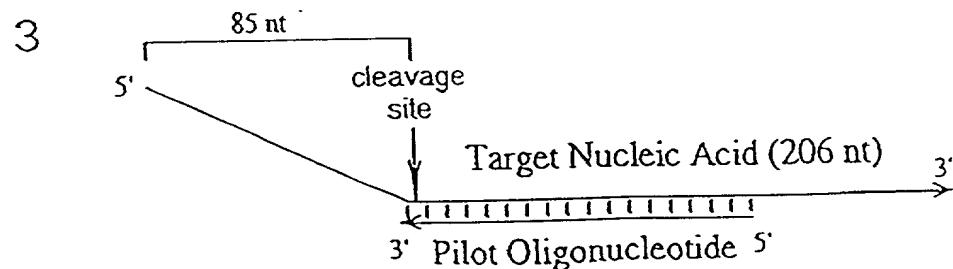
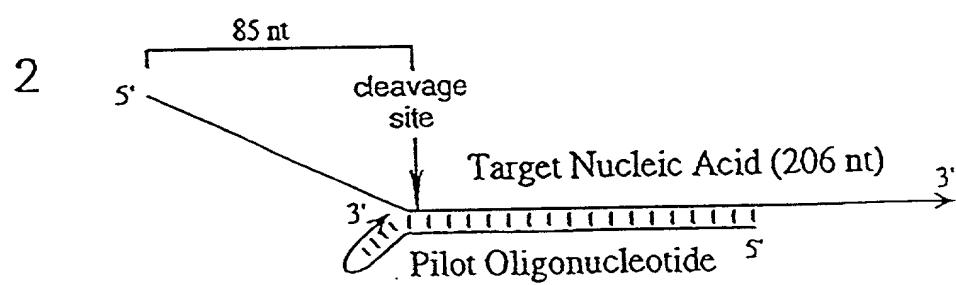
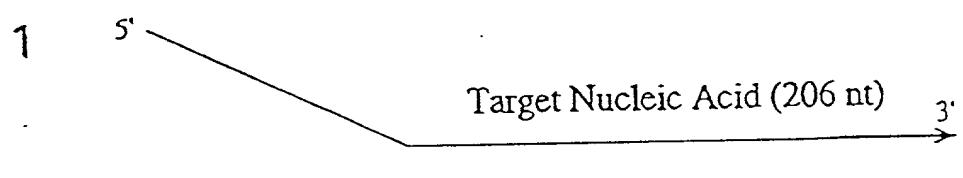


FIGURE 22B.

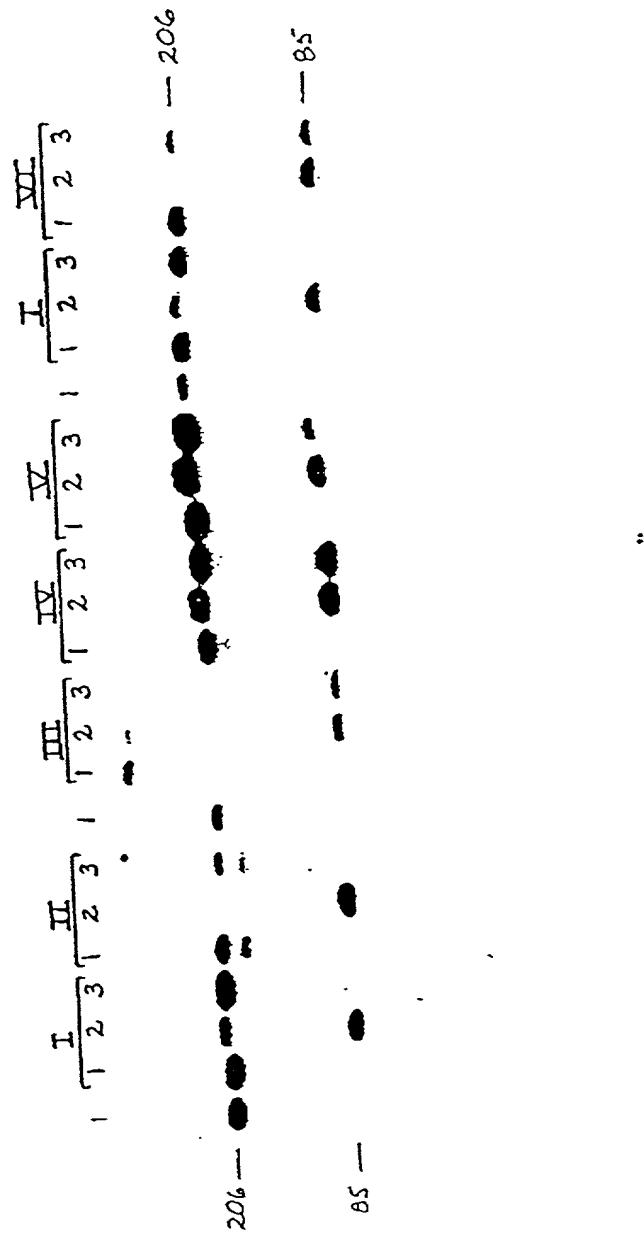


FIGURE 23

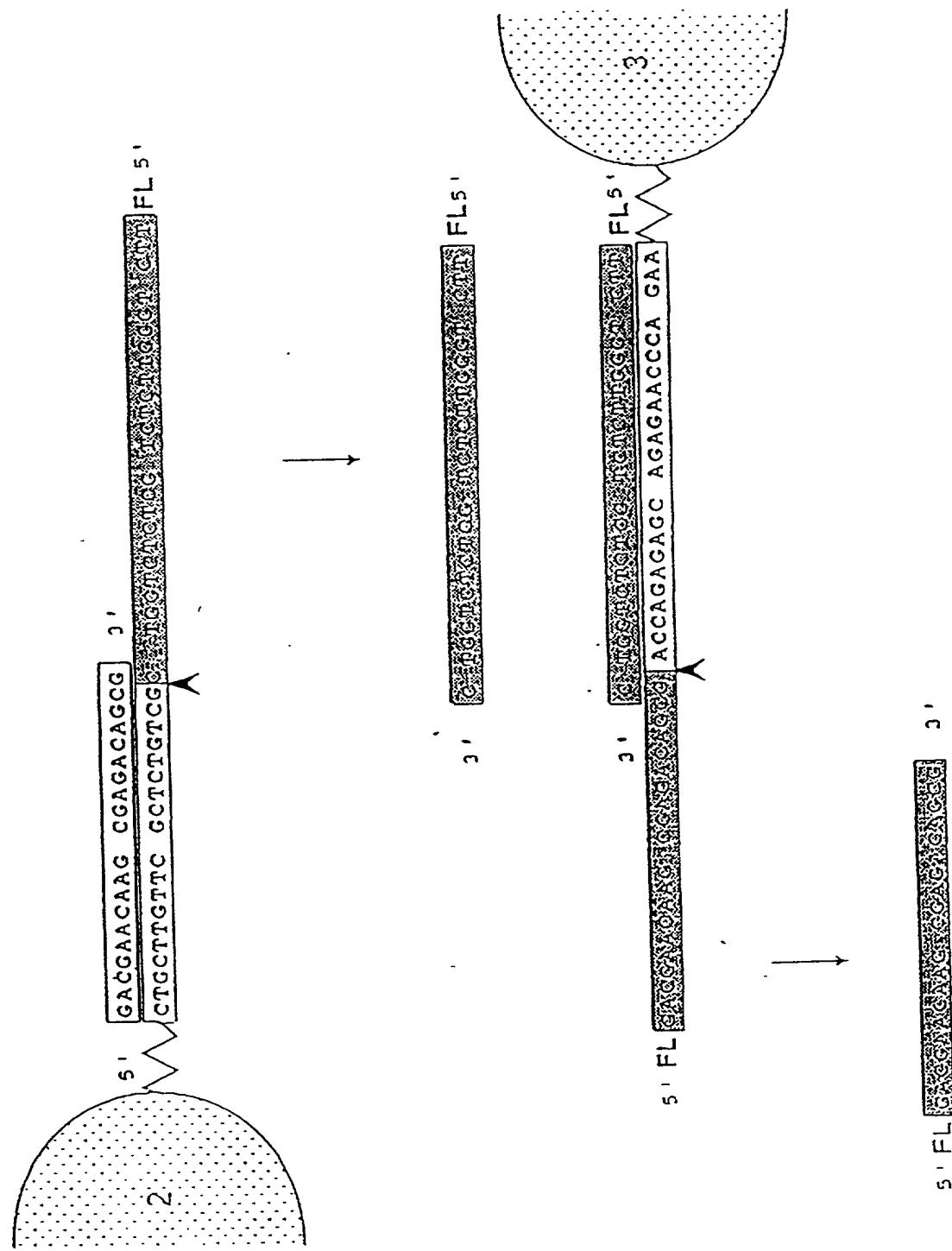


Figure 24 a 20160416

FIGURE 24

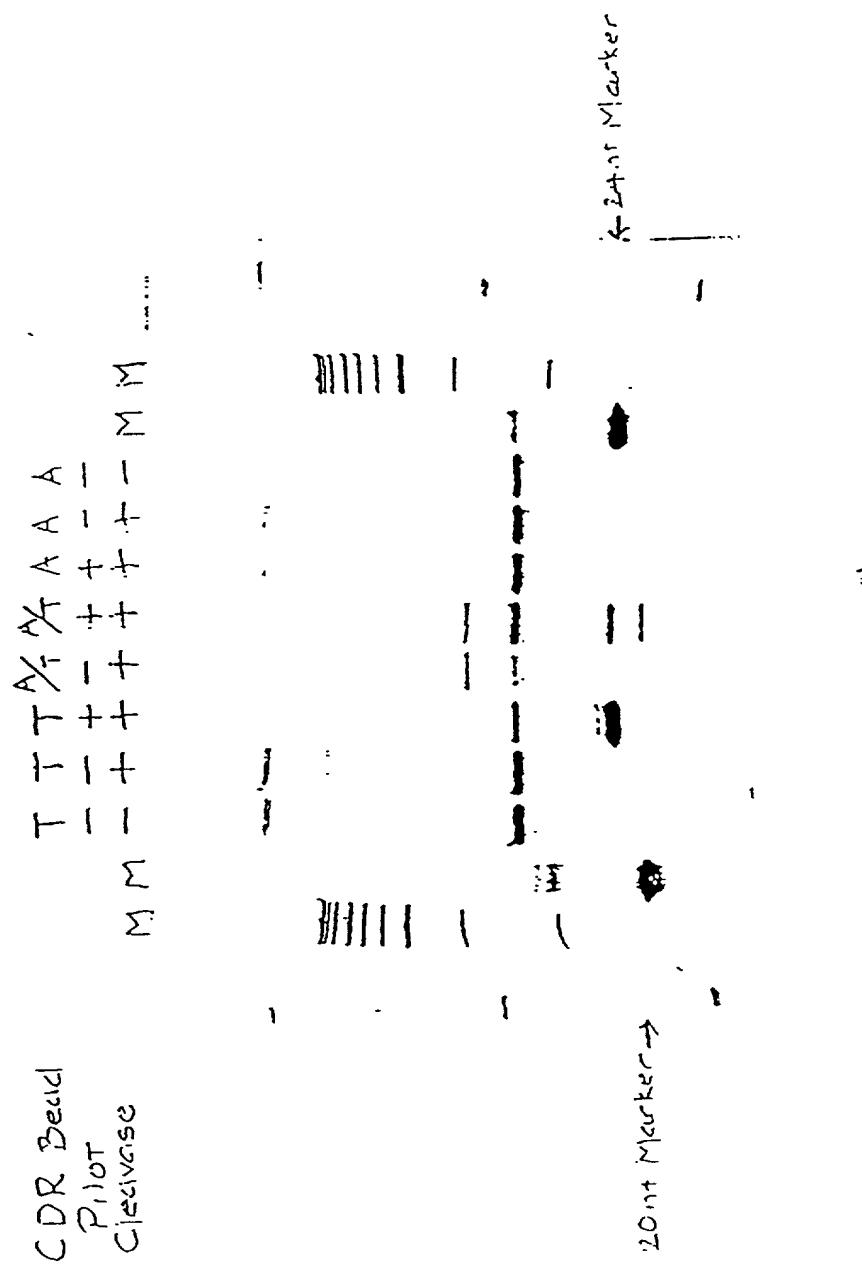
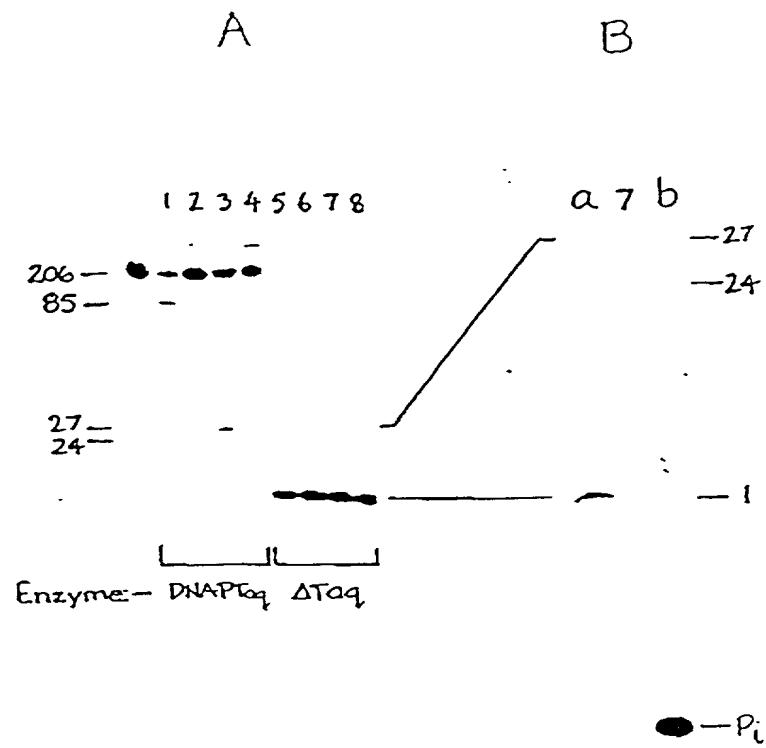


FIGURE 25



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FIGURE 26

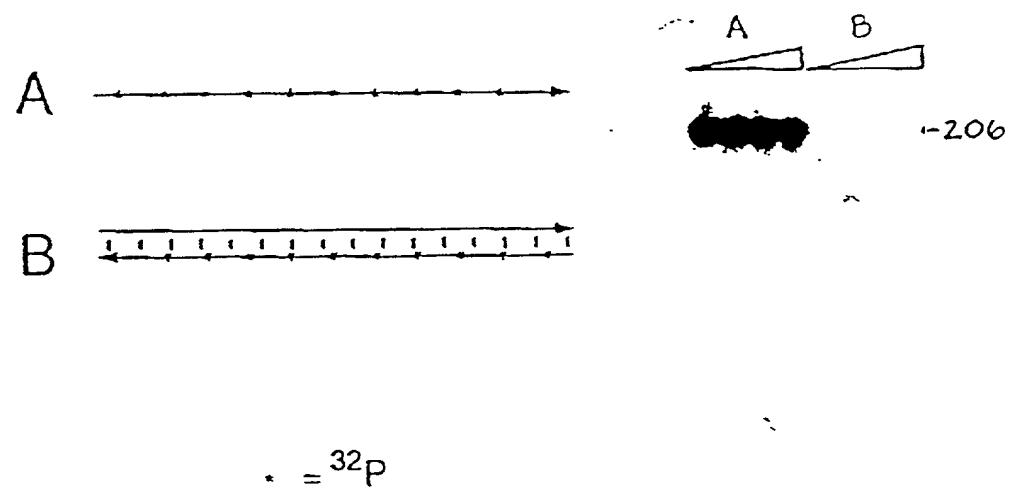


FIGURE 27

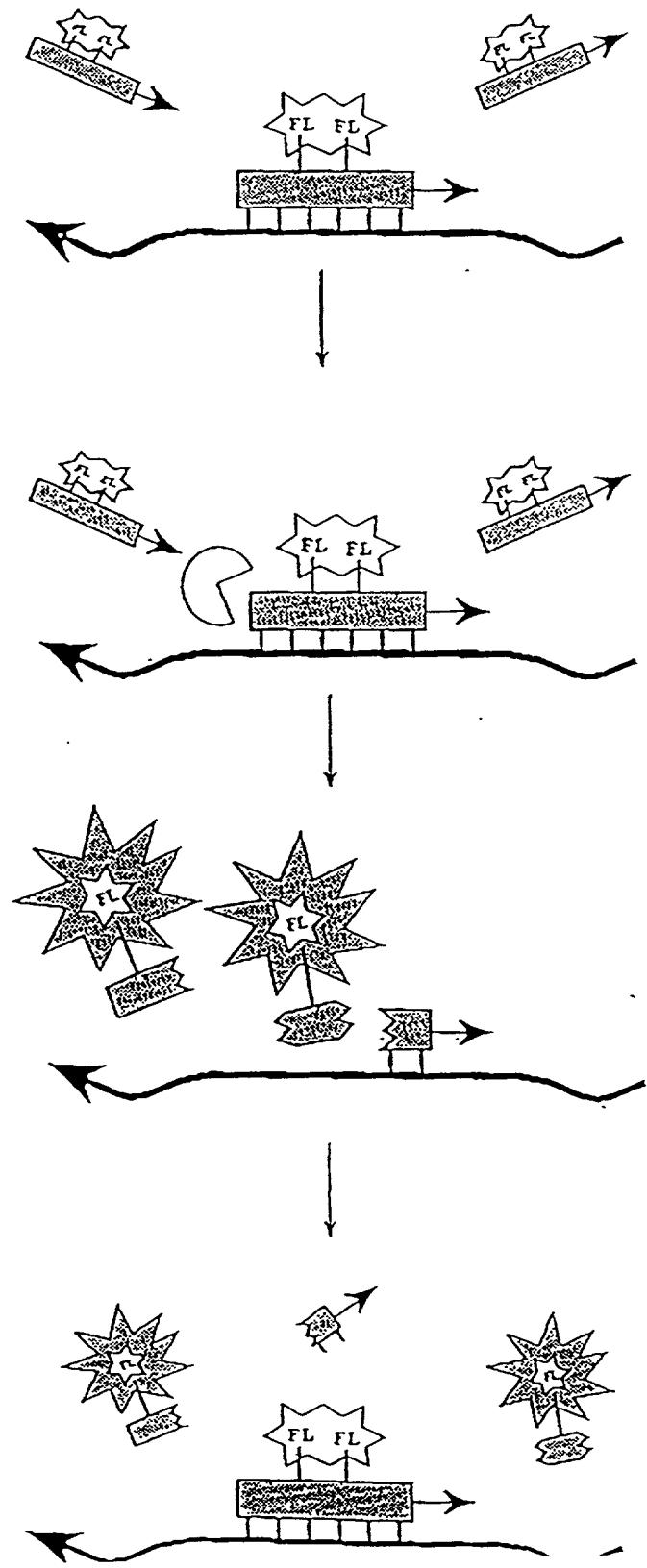
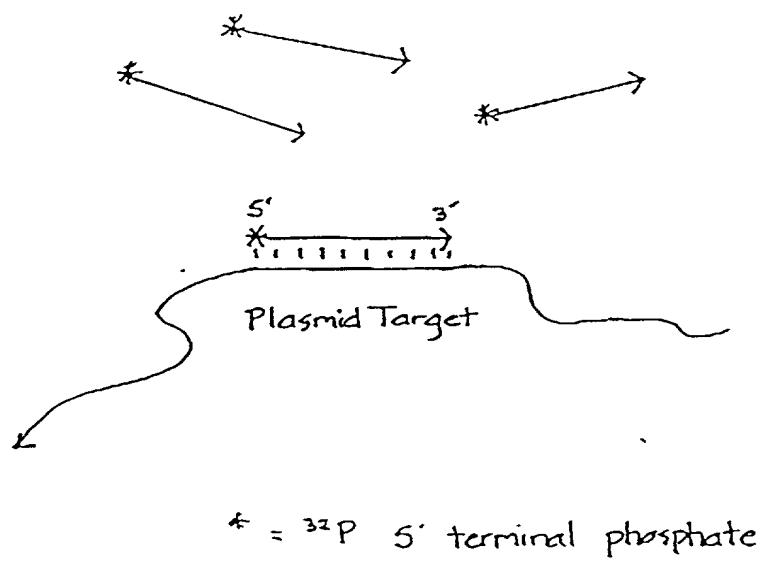


FIGURE 28A



E D E D D D E E D D D D

FIGURE 28B

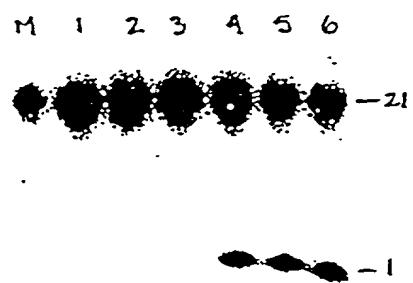


FIGURE 29

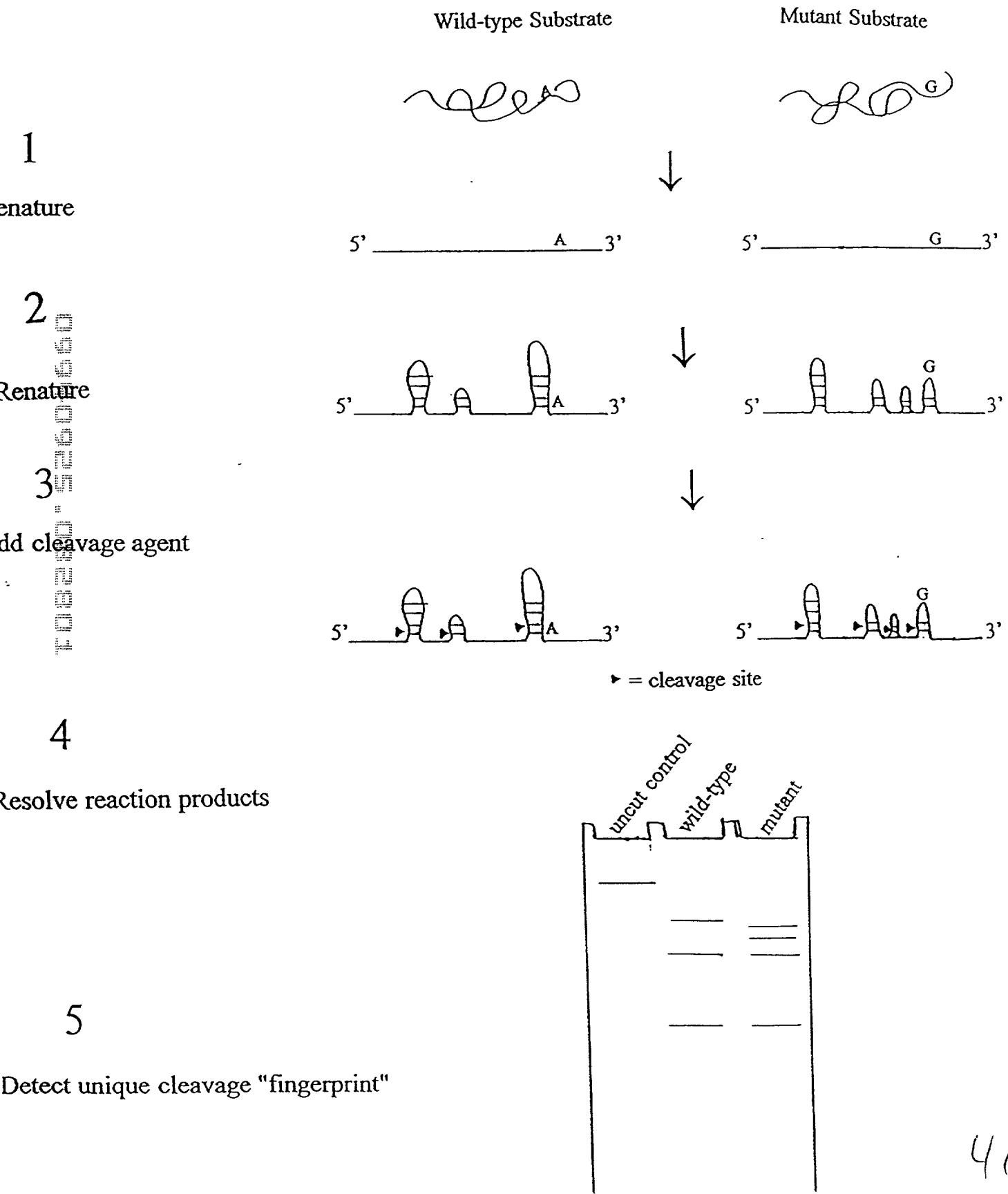
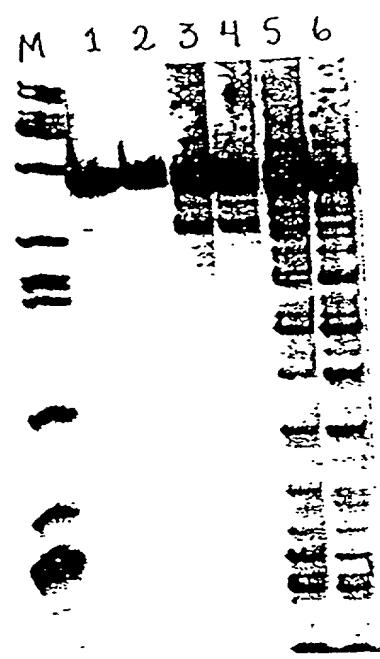


FIGURE 30



70022300 2260041560

42

FIGURE 31

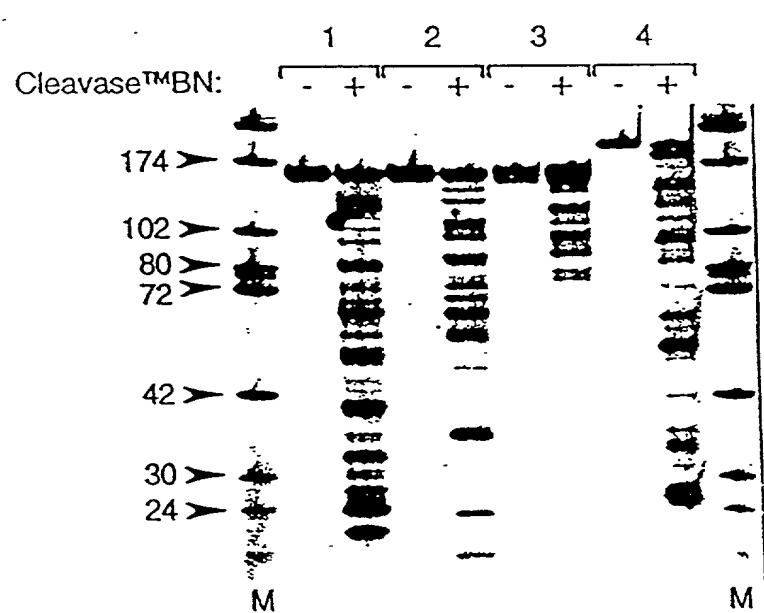


FIGURE 32

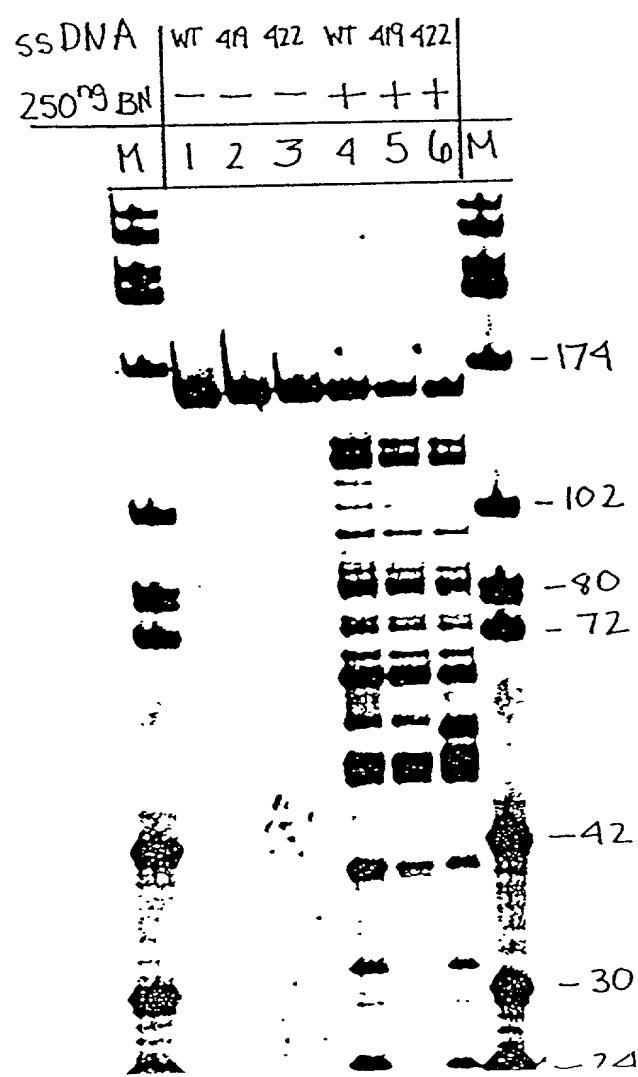
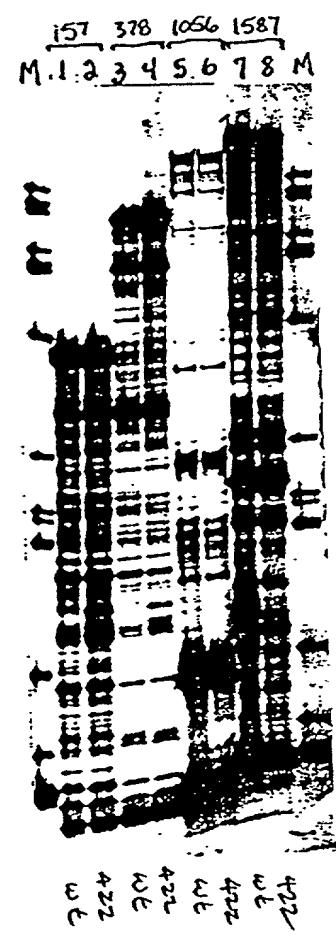
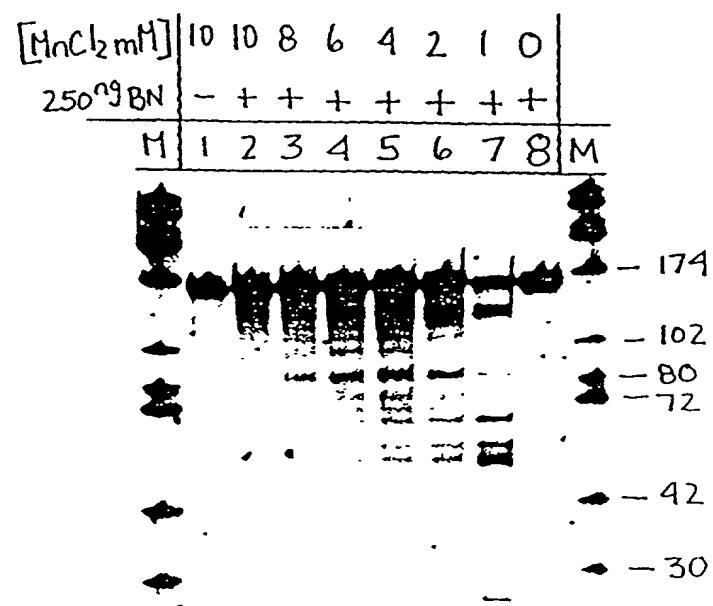


FIGURE 33



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FIGURE 34



70 60 50 40 30 20 10 0

FIGURE 35

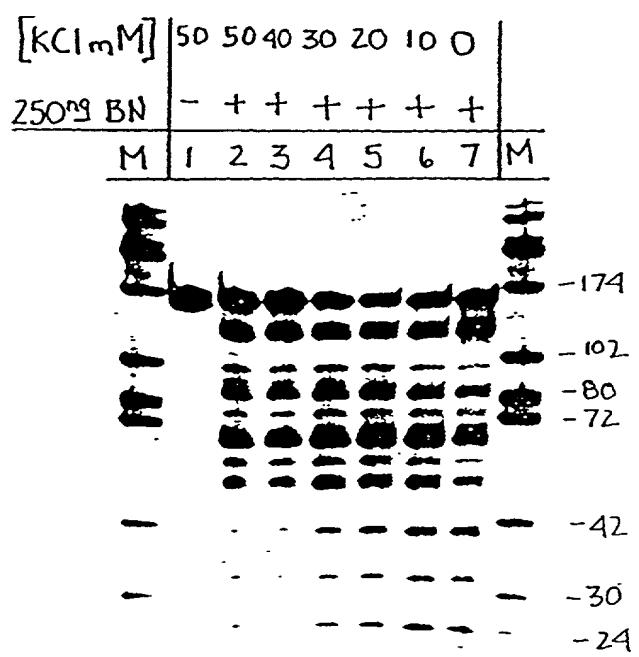


FIGURE 36

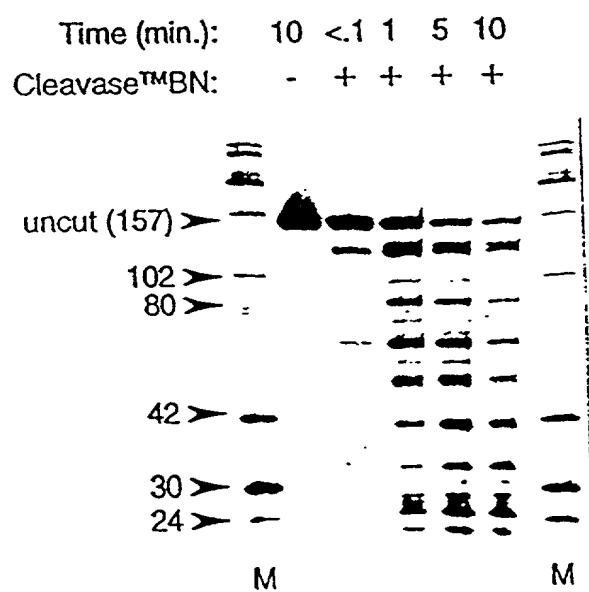


FIGURE 37

TCGEGCGGCGCTGGTGTG

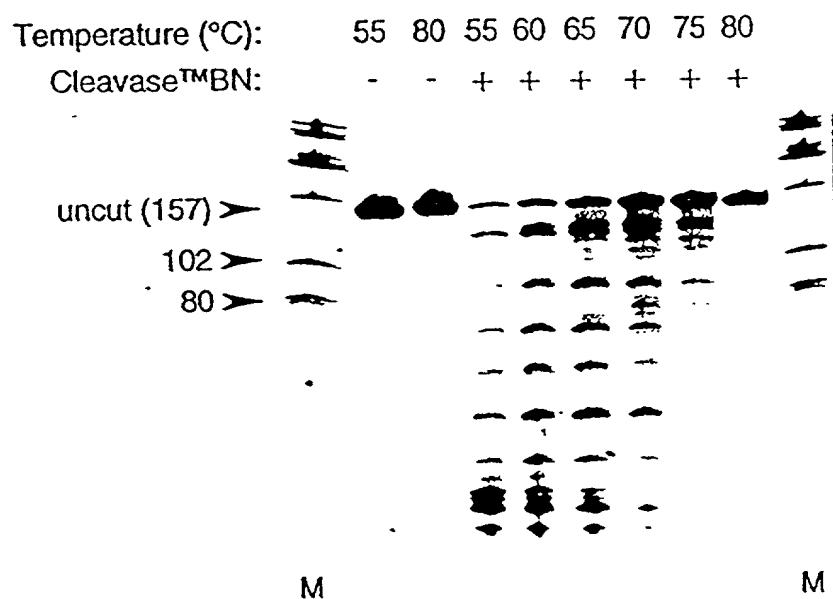
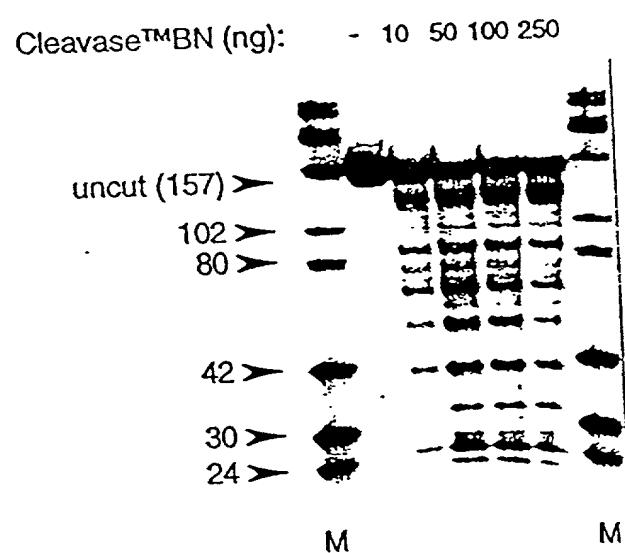


FIGURE 38



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FIGURE 39

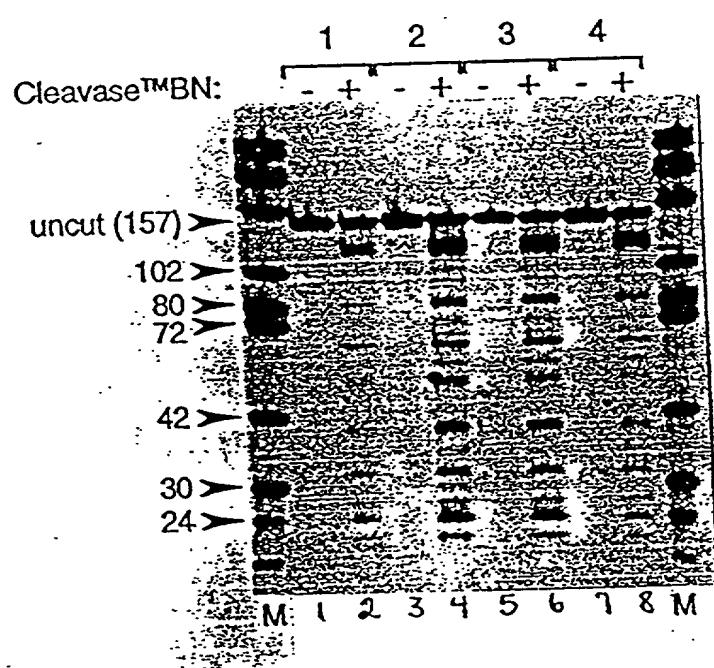
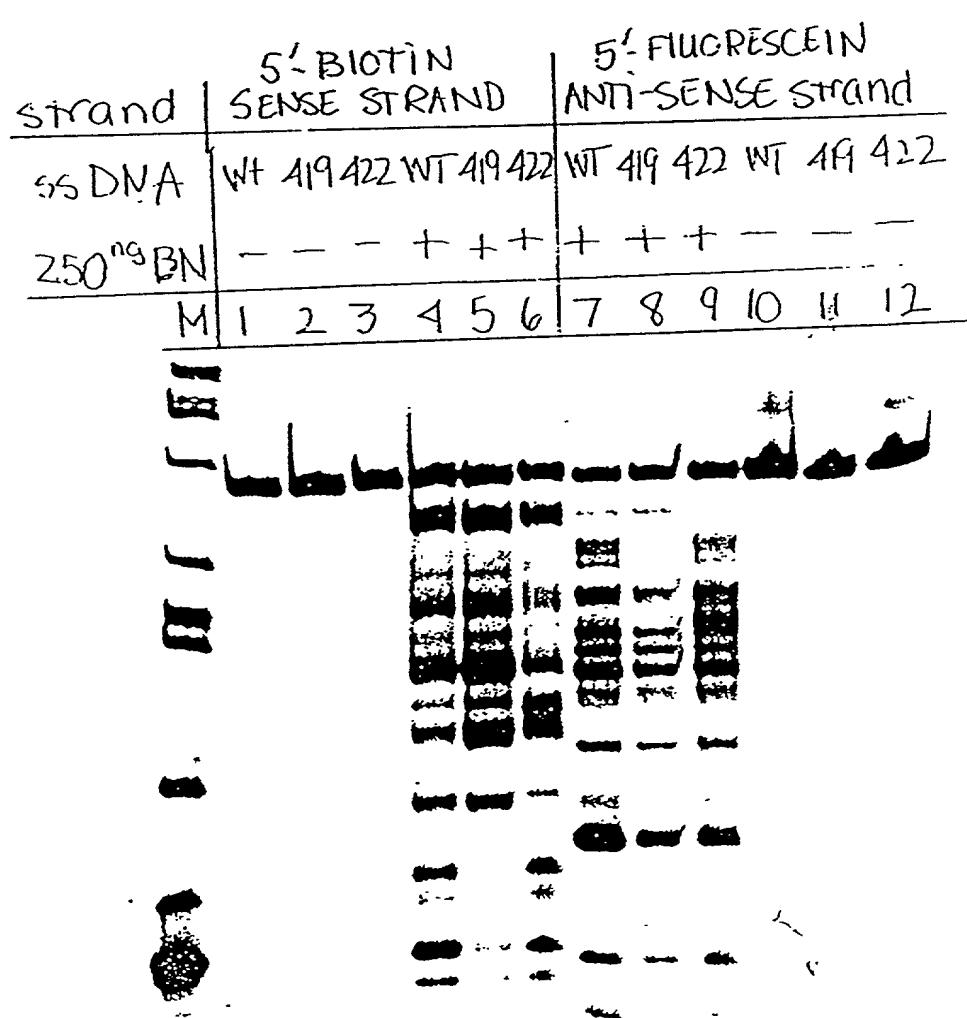
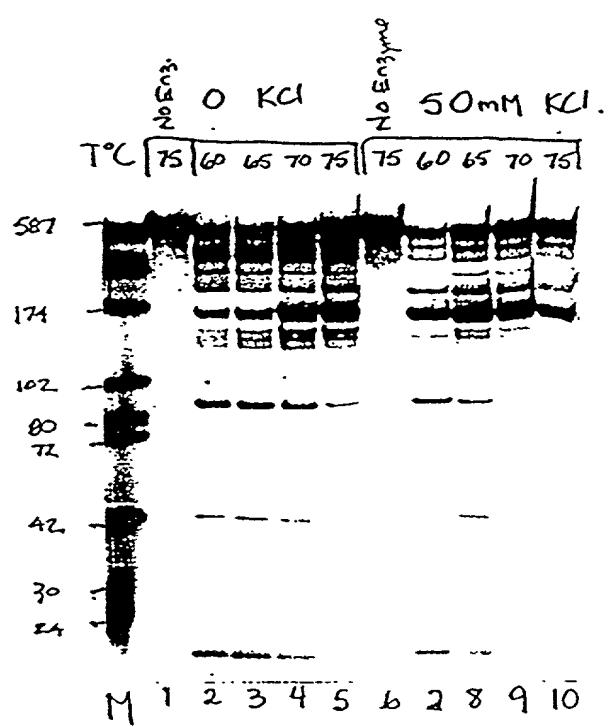


FIGURE 40



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FIGURE 41



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The following table gives the results of the experiments on the effect of the different factors on the rate of absorption.

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FIGURE 42

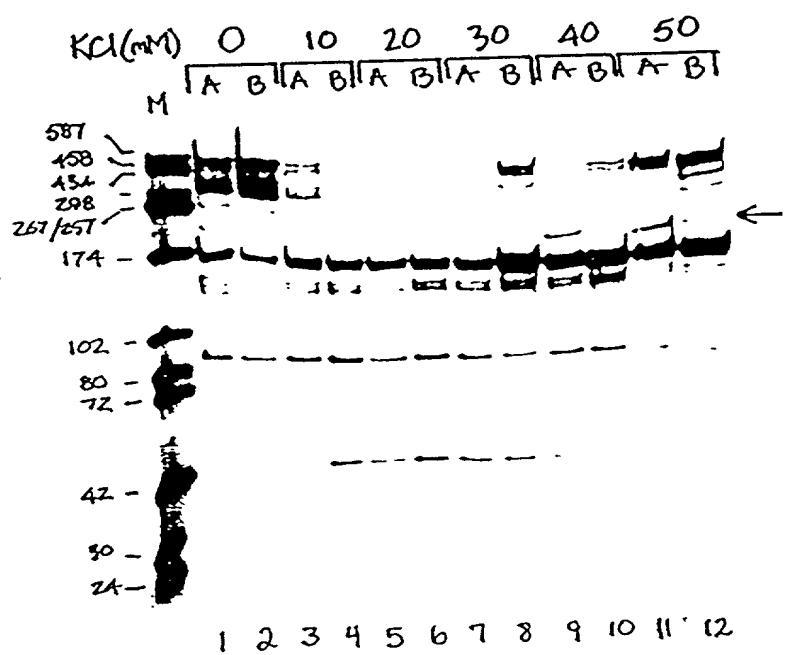
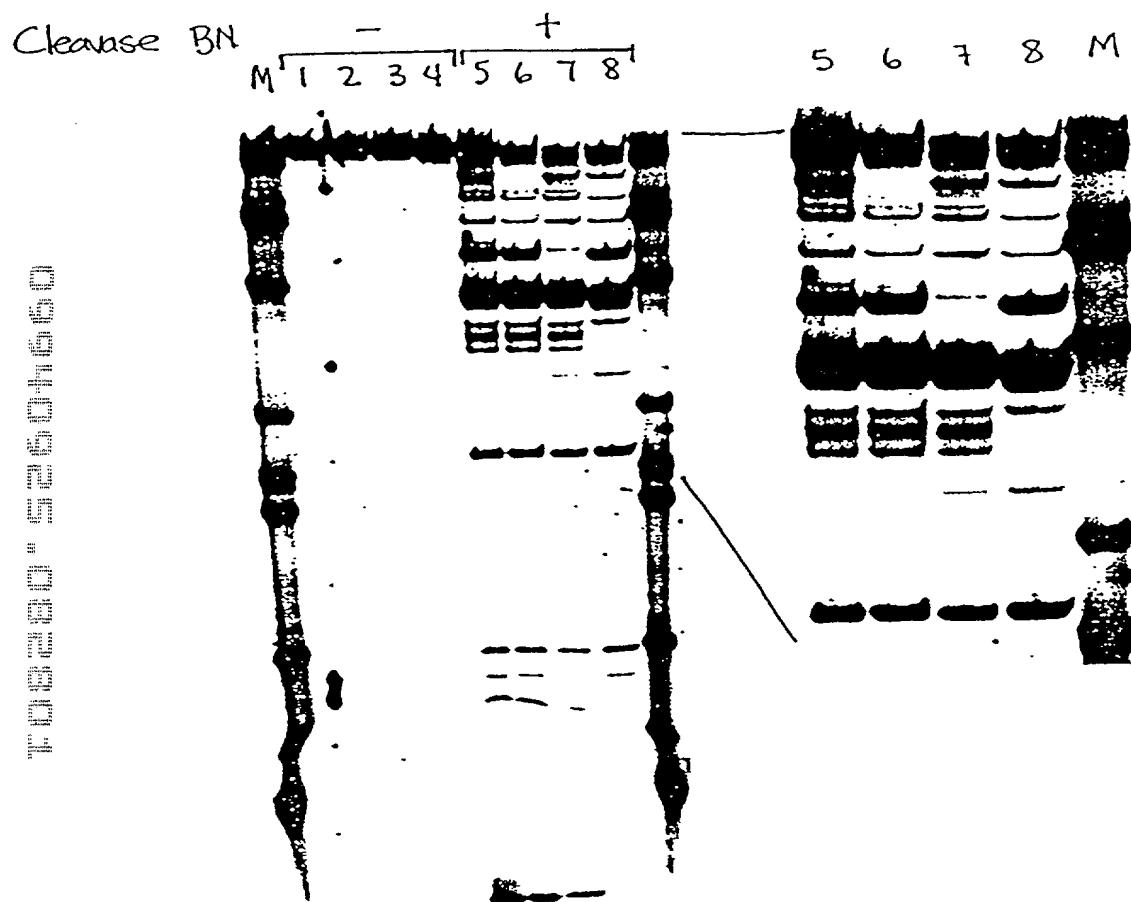


FIGURE 43



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FIGURE 44

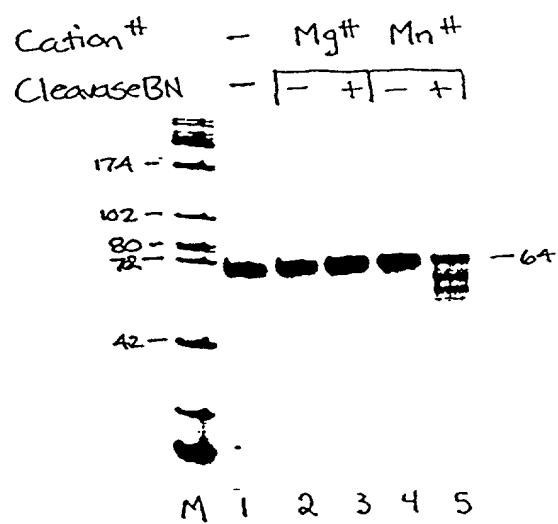
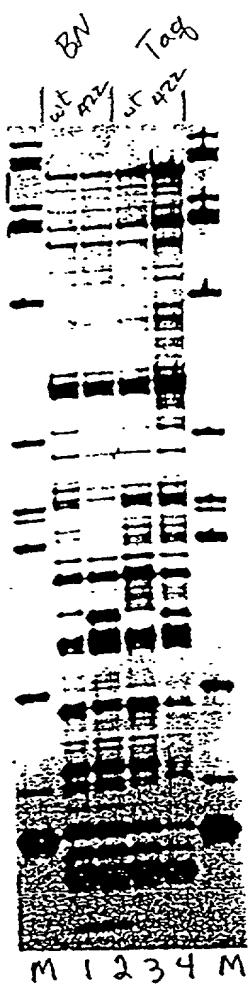


FIGURE 45



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FIGURE 46

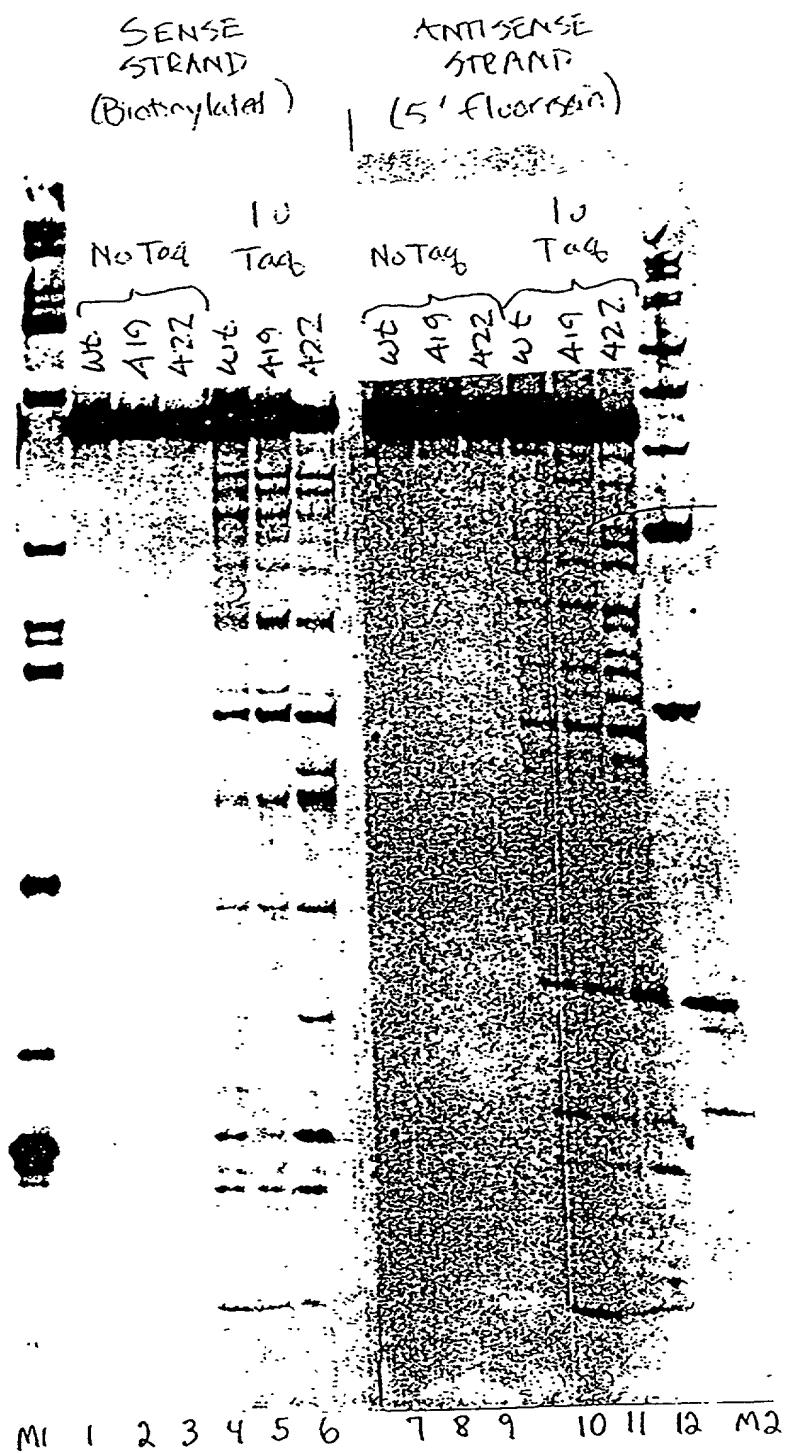


FIGURE 47

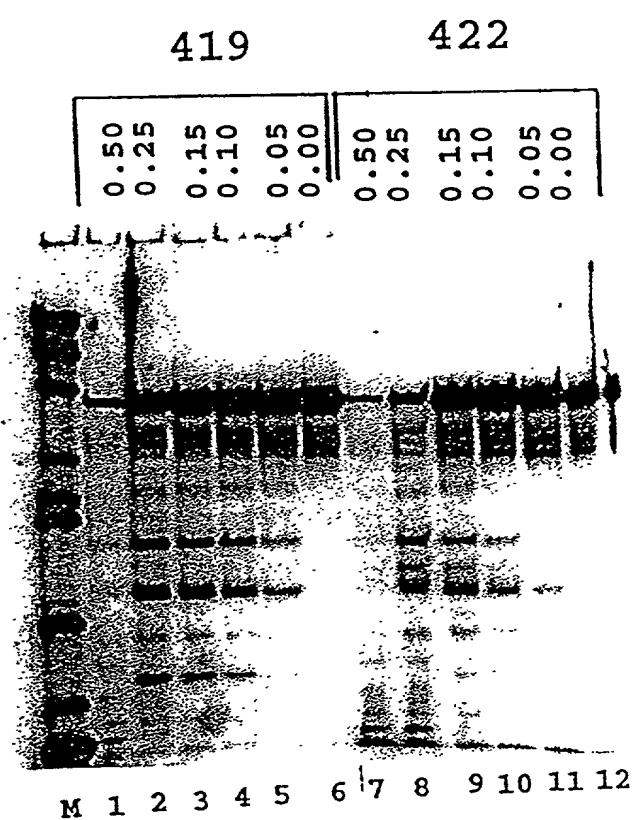
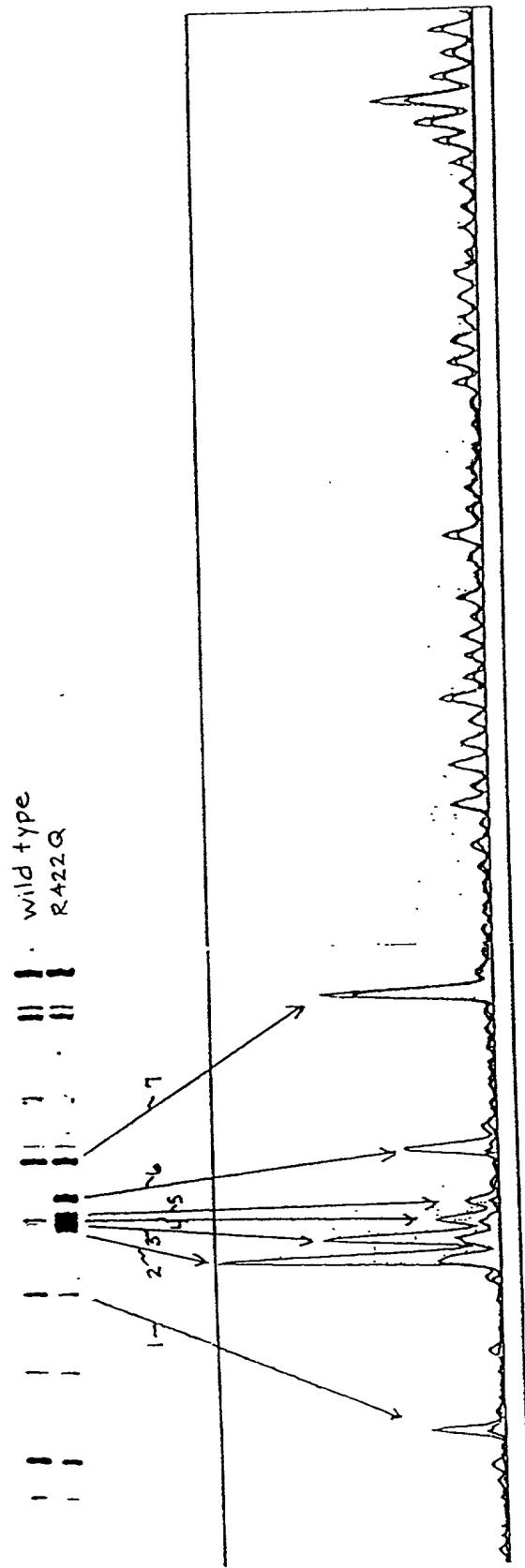


FIGURE 48

T 0 3 2 8 0 " E 2 6 0 + 6 6 0



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100 . 8 - 1	5' TGATGTTAAATACTGCATTTCGCTCTGTATTCA GTGCCCTGGGA 3' ACTACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	150	5' GGGCTGGCAGATTGAGCCCTGGGA 3' ACTACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	200
46 . 16 - 10	5' TGATGTTAAATACTGCATTTCGCTCTGTATTCA GTGCCCTGGGA 3' ACTACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	46 . 16 - 12	5' TGATGTTAAATACTGCATTTCGCTCTGTATTCA GTGCCCTGGGA 3' ACCACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	46 . 16 - 12
19 . 16 - 3	5' TGATGTTAAATACTGCATTTCGCTCTGTATTCA GTGCCCTGGGA 3' ACTACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	CBM / 251	5' TGATGTTAAATACTGCATTTCGCTCTGTATTCA GTGCCCTGGGA 3' ACTACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	19 . 16 - 3
CBM / 251	5' TGATGTTAAATACTGCATTTCGCTCTGTATTCA GTGCCCTGGGA 3' ACTACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	CBM / 251	5' TGATGTTAAATACTGCATTTCGCTCTGTATTCA GTGCCCTGGGA 3' ACTACATATTATAAGTGA CGTAAGCGAGACATAAAGTCA	CBM / 251

L.100.8-1 5' AGCCCTGGTTCCTGGTAGACTCTACCAAGGACTTGTGTTAACAGACCTCTTCATAAAAGCTGCC
 (SEQ ID NO: 76) 3' TCGGACCCACAAGGGACGATCTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCACCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG

L.46.16-10 5' AGCCCTGGGTTCCTGGTAGACTCTACCAAGGACTTGTGTTAACAGACCTCTTCATAAAAGCTGCC
 (SEQ ID NO: 77) 3' TCGGACCCACAAGGGACGATCTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCACCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG

L.46.16-12 5' AGCCCTGGGTTCCTGGTAGACTCTACCAAGGACTTGTGTTAACAGACCTCTTCATAAAAGCTGCC
 (SEQ ID NO: 78) 3' TCGGACCCACAAGGGACGATCTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCACCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG

L.19.16-3 5' AGCCCTGGGTTCCTGGTAGACTCTACCAAGGACTTGTGTTAACAGACCTCTTCATAAAAGCTGCC
 (SEQ ID NO: 79) 3' TCGGACCCACAAGGGACGATCTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCACCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG

L.CEM/251 5' AGCCCTGGGTTCCTGGTAGACTCTACCAAGGACTTGTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCACCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG
 (SEQ ID NO: 80) 3' TCGGACCCACAAGGGACGATCTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCACCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG

L.36.8-3 5' AGCCCTGAGTGTTCCTGCTAAACTCTACCAAGGACTTGTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCGCCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG
 (SEQ ID NO: 81) 3' TCGGACTCAAGGGACGATCTGAGAGTGGTCCGTGAAACCGAACCCC GTCTCGCCGAGGTGGAAACGAATTTCCTGGAGAAGTTATTTCGACGG

↓ Hairpin ↓

L.100.8-1 5' ATTTTAGAAGTAGGGCCAAAGTGTGTGTTCCTCCATCTCTCCATAGCCCCCGCCCTG G 3'
 3' TAAAATCTTCATCCGGTCACACACAAGGGTAGAGGGATCGGGGGGAC C 5'

L.46.16-10 5' ATTTTAGAAGTAGGGCCAAAGTGTGTGTTCCTCCATCTCTCCATAGCCCCCGCCCTG G 3'
 3' TAAAATCTTCATCCGGTCACACACAAGGGTAGAGGGATCGGGGGGAC C 5'

L.46.16-12 5' ATTTTAGAAGTAGGGCCAAAGTGTGTGTTCCTCCATCTCTCCATAGCCCCCGCCCTG G 3'
 3' TAAAATCTTCATCCGGTCACACACAAGGGTAGAGGGATCGGGGGGAC C 5'

L.19.16-3 5' ATTTTAGAAGTAGGGCCAAAGTGTGTGTTCCTCCATCTCTCCATAGCCCCCGCCCTG G 3'
 3' TAAAATCTTCATCCGGTCACACACAAGGGTAGAGGGATCGGGGGGAC C 5'

L.CEM/251 5' ATTTTAGAAGTAGGGCCAAAGTGTGTGTTCCTCCATCTCTCCATAGCCCCCGCCCTG G 3'
 3' TAAAATCTTCATCCGGTCACACACAAGGGTAGAGGGATCGGGGGGAC C 5'

L.36.8-3 5' ATTTTAGAAGTAGGGCCAAAGTGTGTGTTCCTCCATCTCTCCATAGCCCCCGCCCTG G 3'
 3' TAAAATCTTCATCCGGTCACACACAAGGGTAGAGGGATCGGGGGGAC C 5'

FIGURE 50

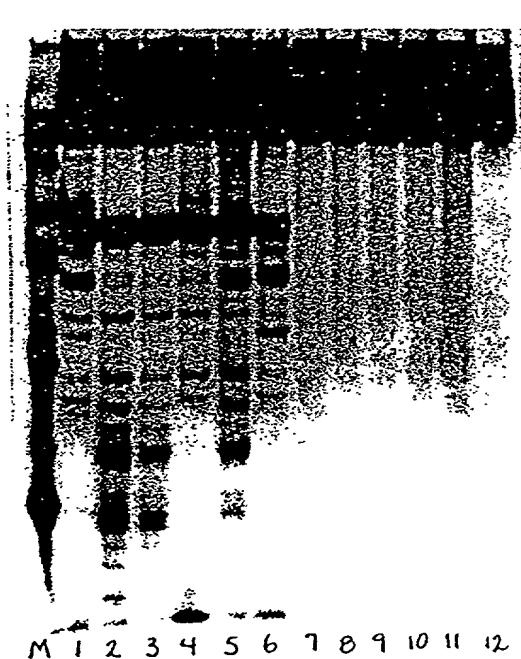


FIGURE 51

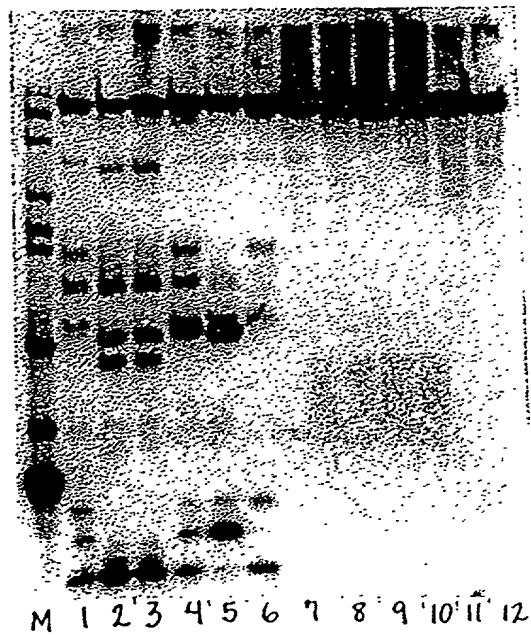
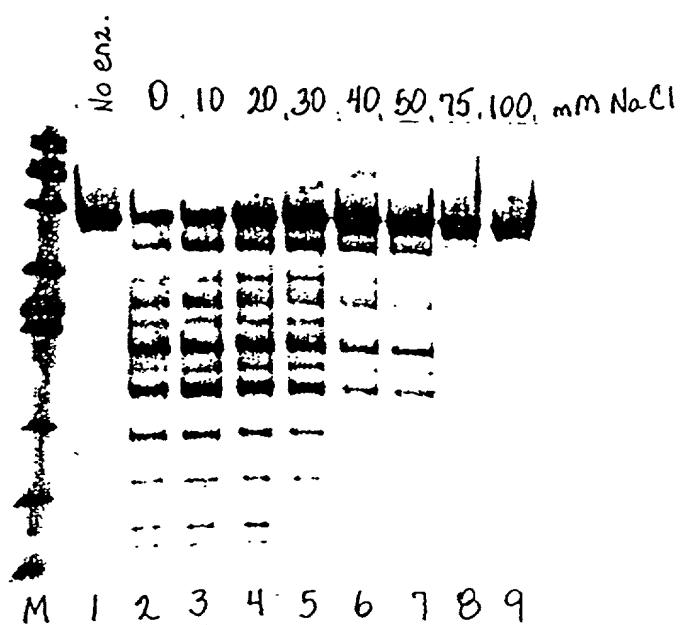


FIGURE 52



45

FIGURE 53

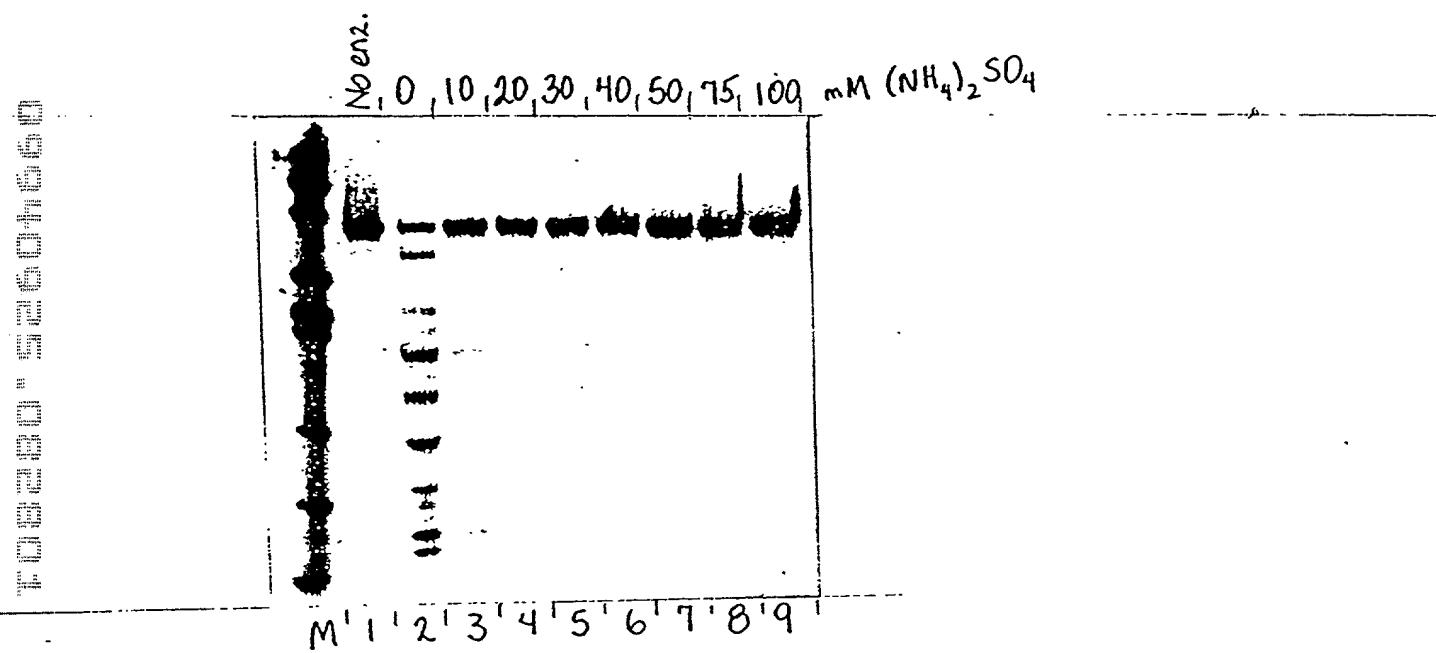


FIGURE 54

T-DNA 200 " Seg 50 + 560

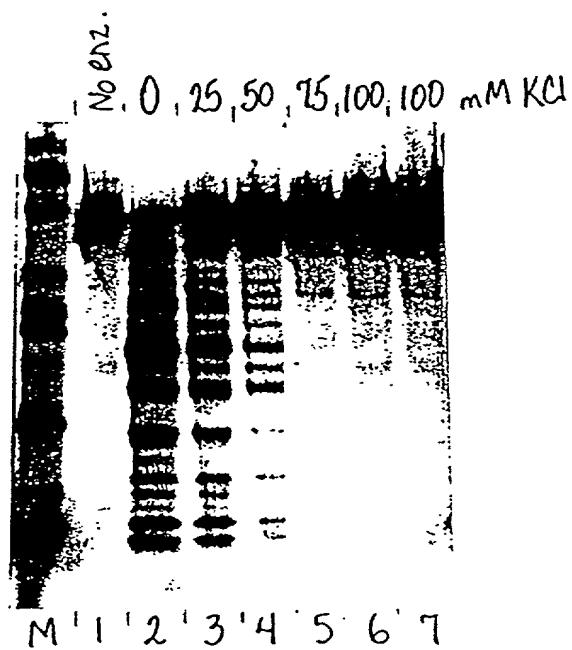


FIGURE 55

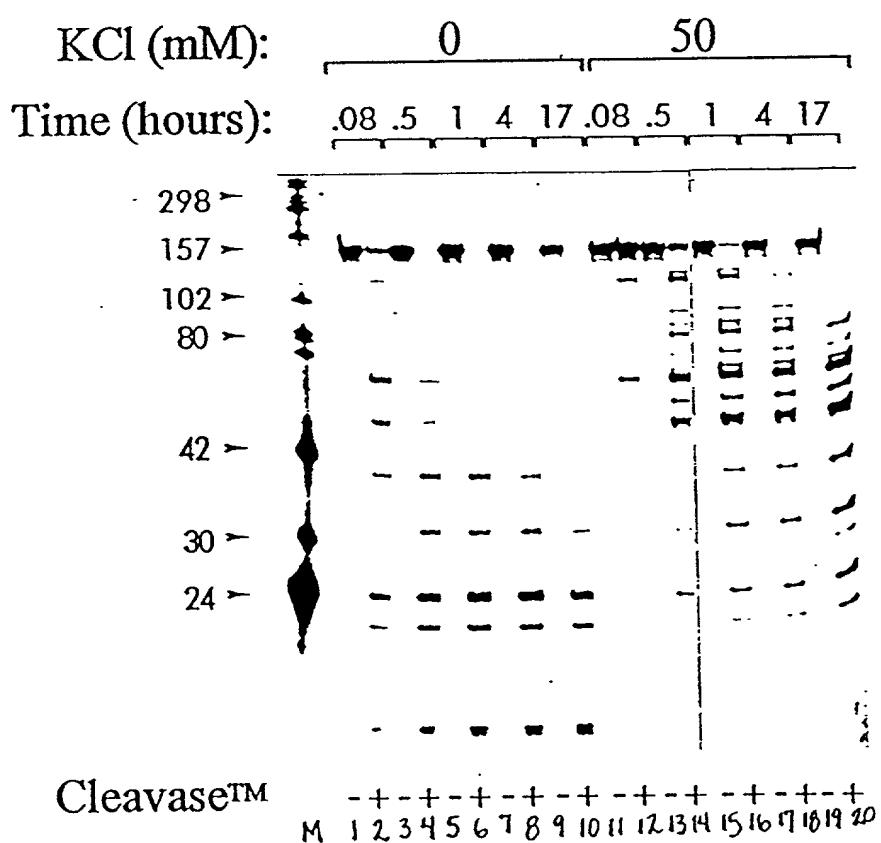


FIGURE 56

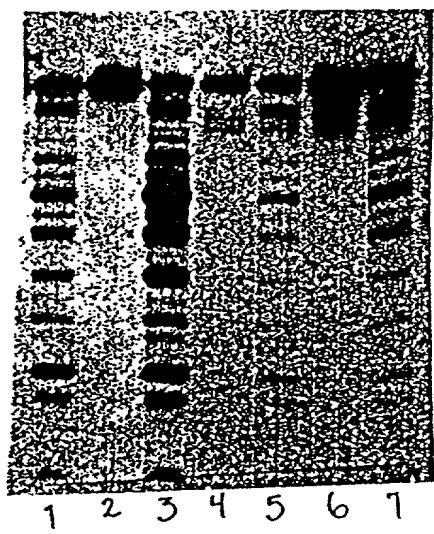


FIGURE 57

FIGURE 57

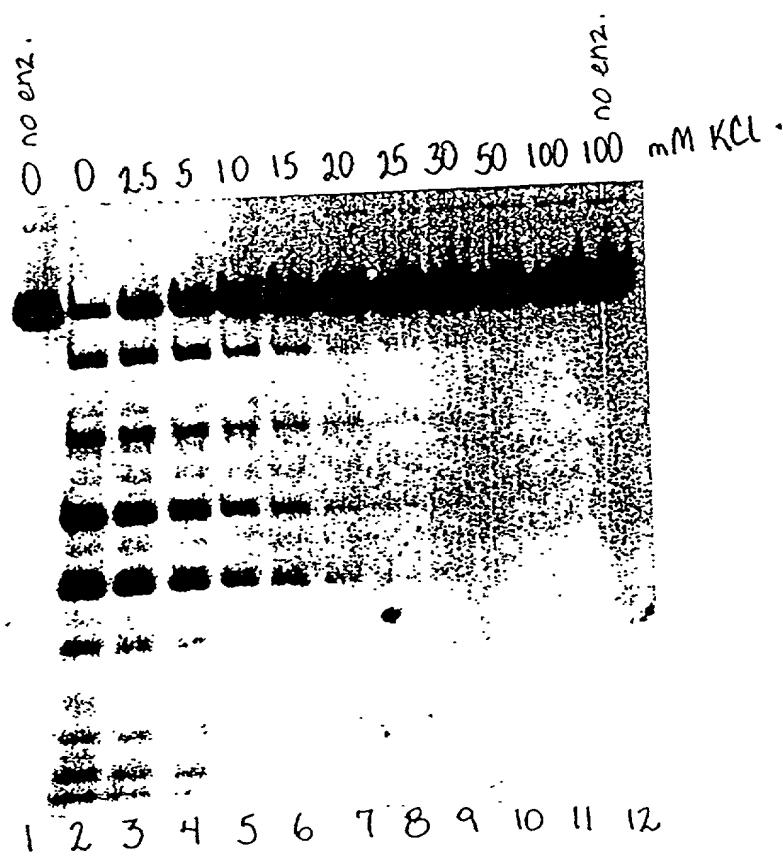


FIGURE 58

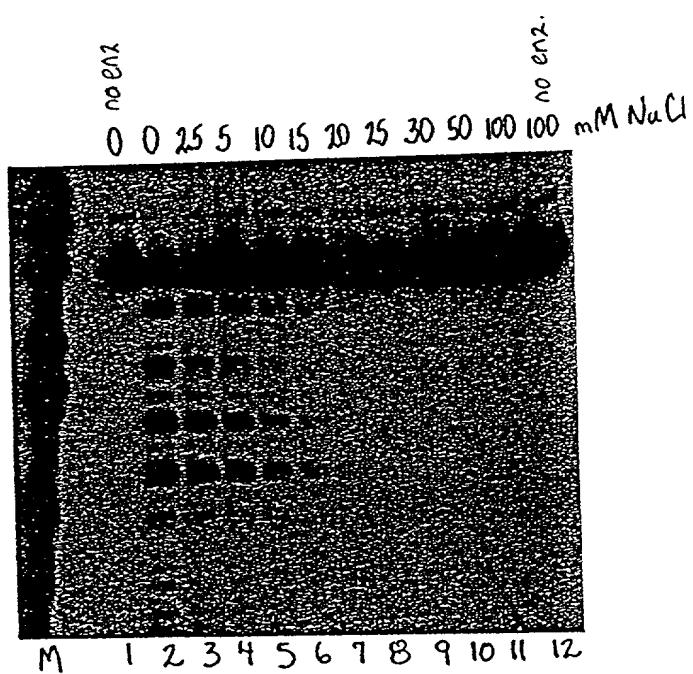


FIGURE 59

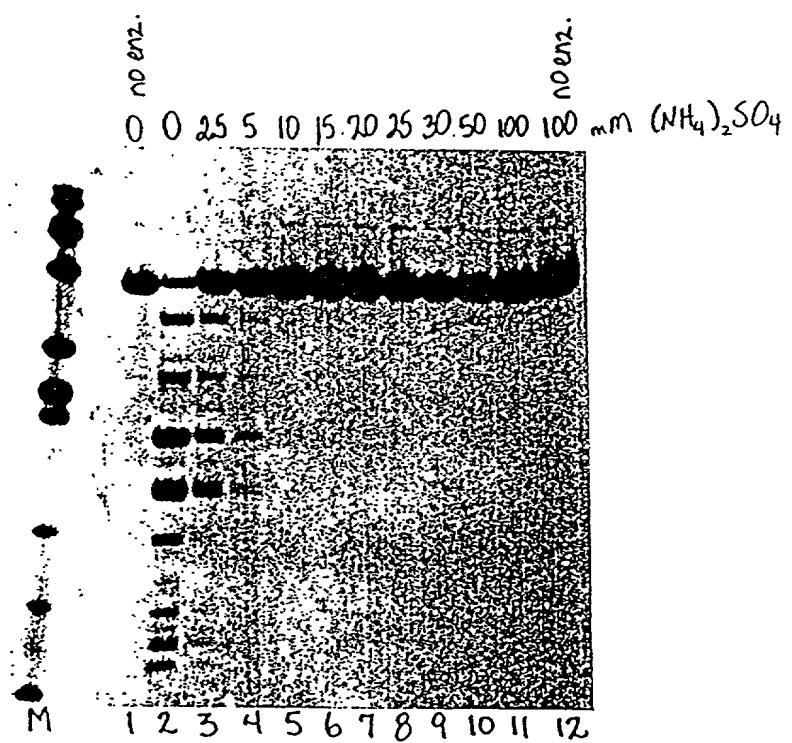


FIGURE 60

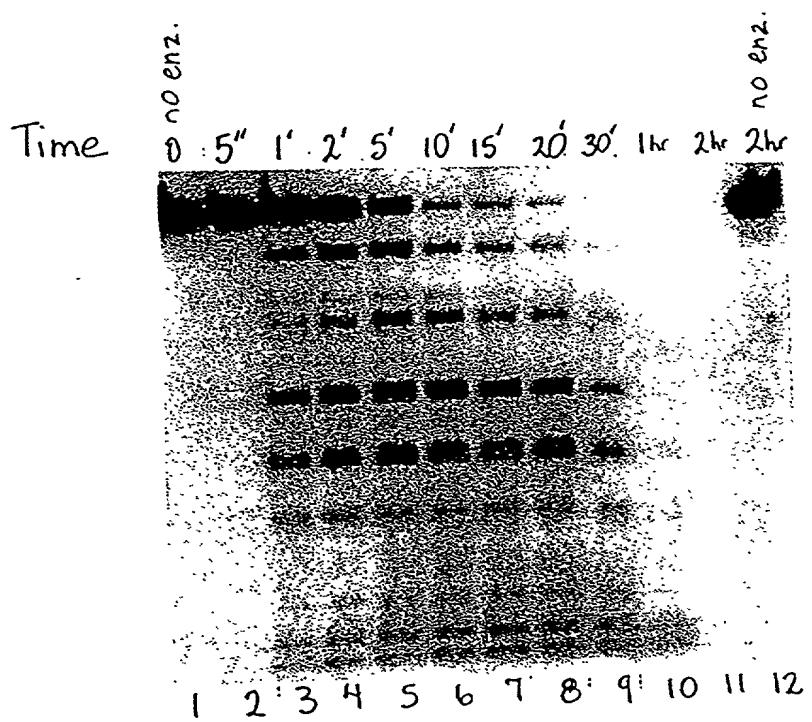


FIGURE 61

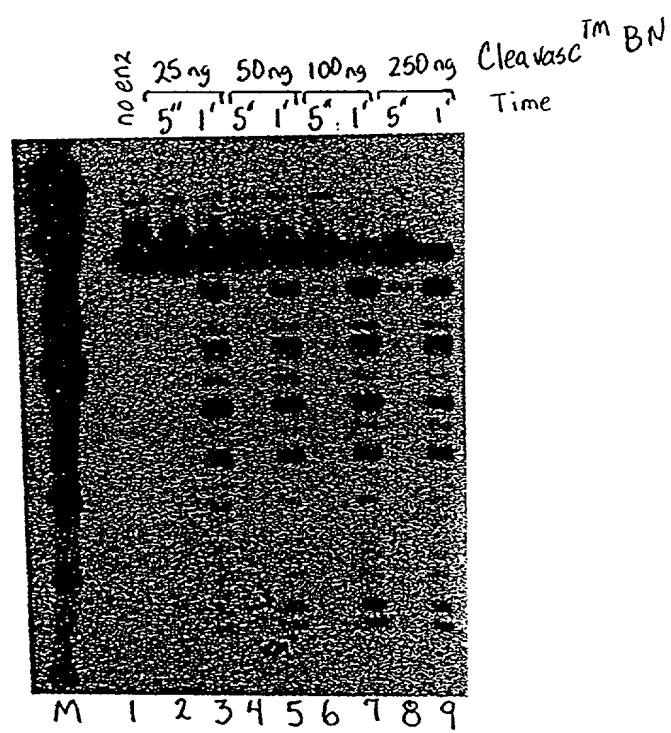
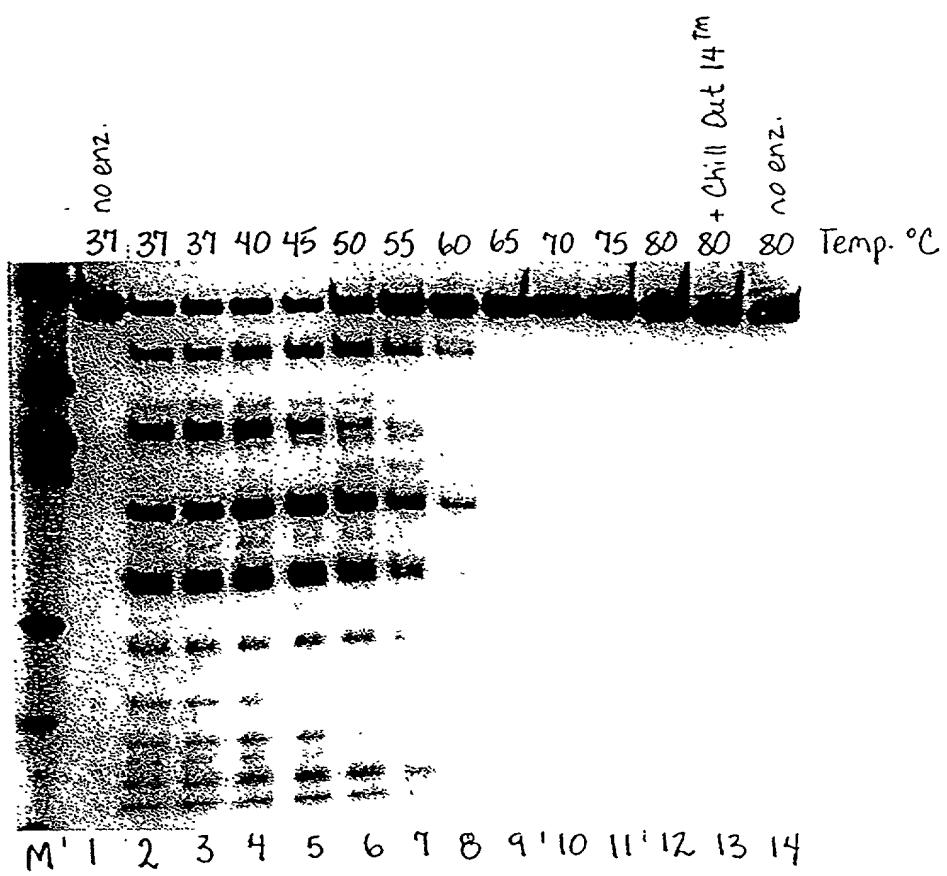


FIGURE 62



75

FIGURE 63

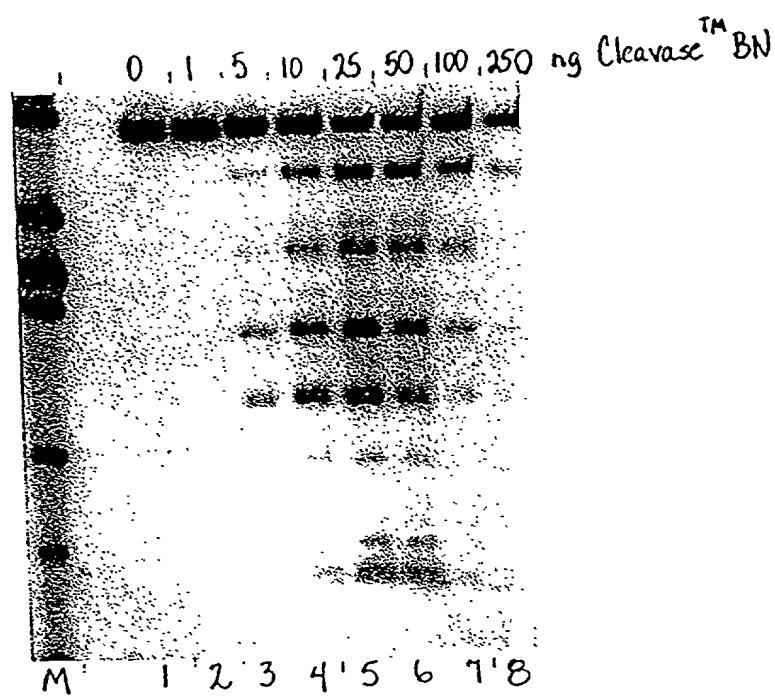
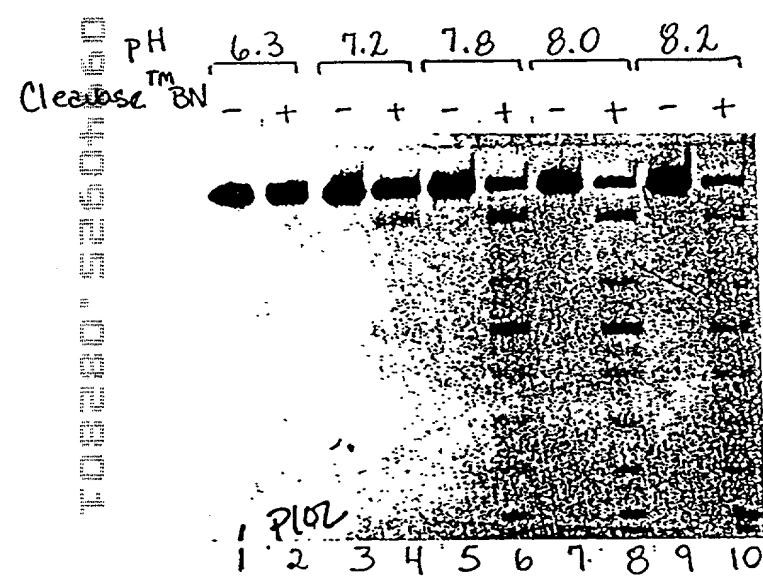
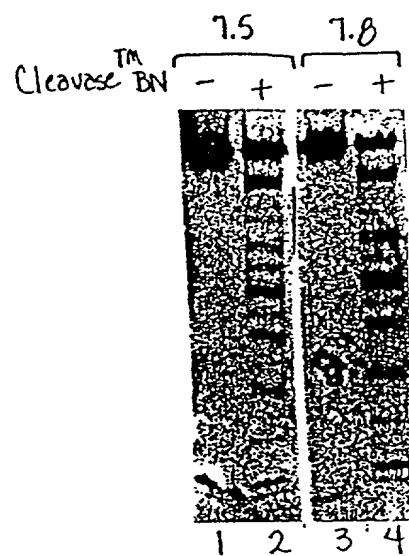


FIGURE 64

A



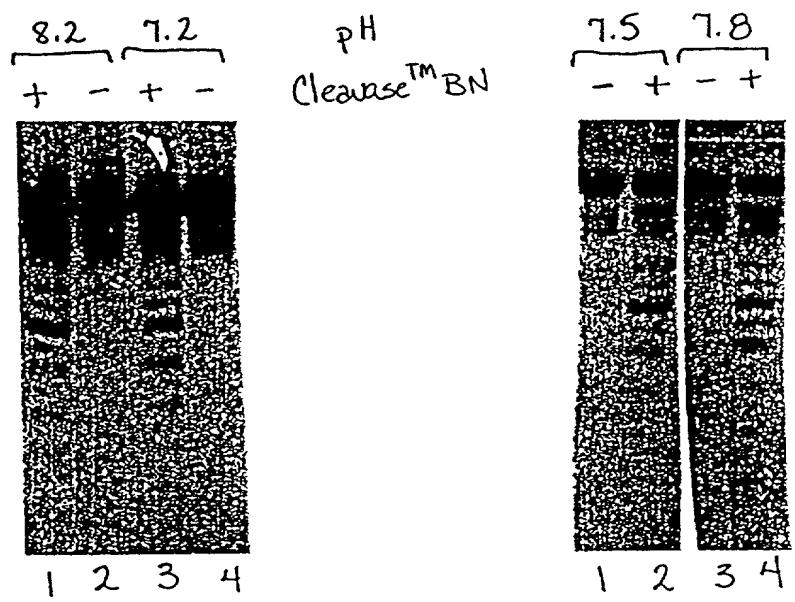
B



77

FIGURE 65

A



B

78

FIGURE 66

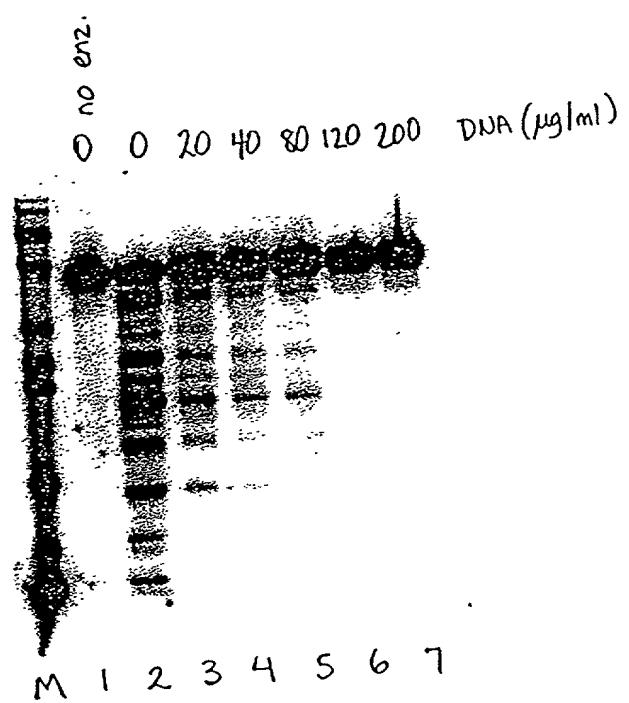
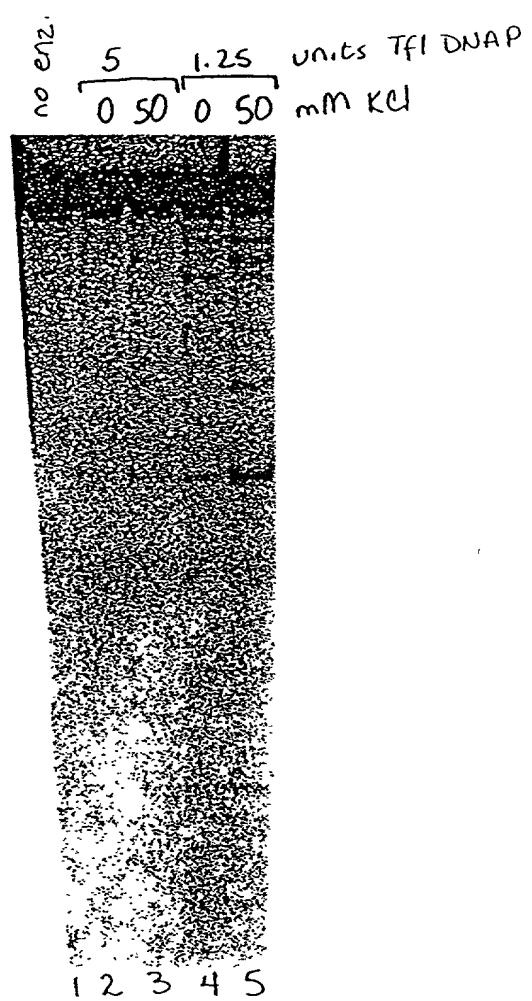


FIGURE 67



80

FIGURE 68

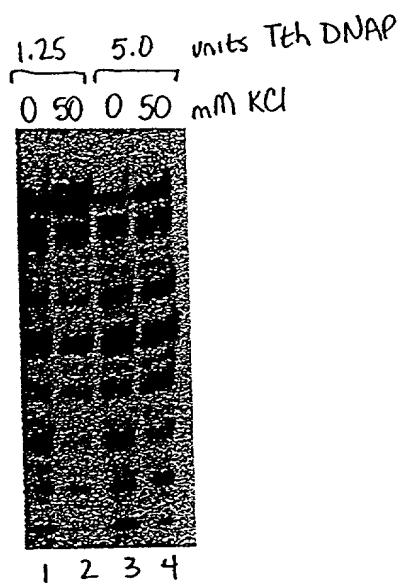


FIGURE 69

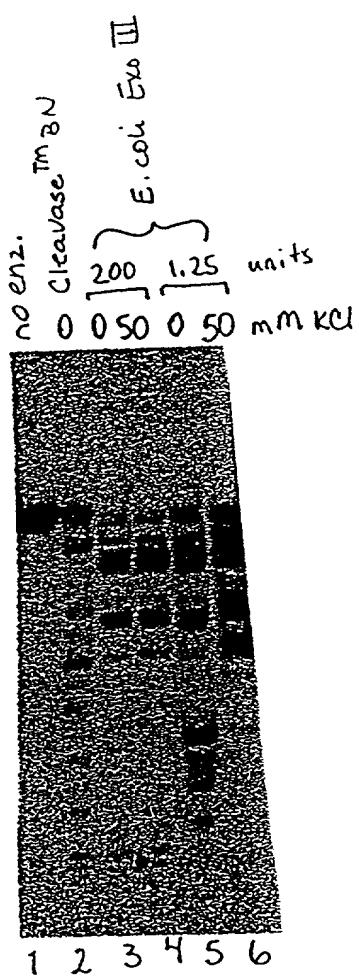


FIGURE 70

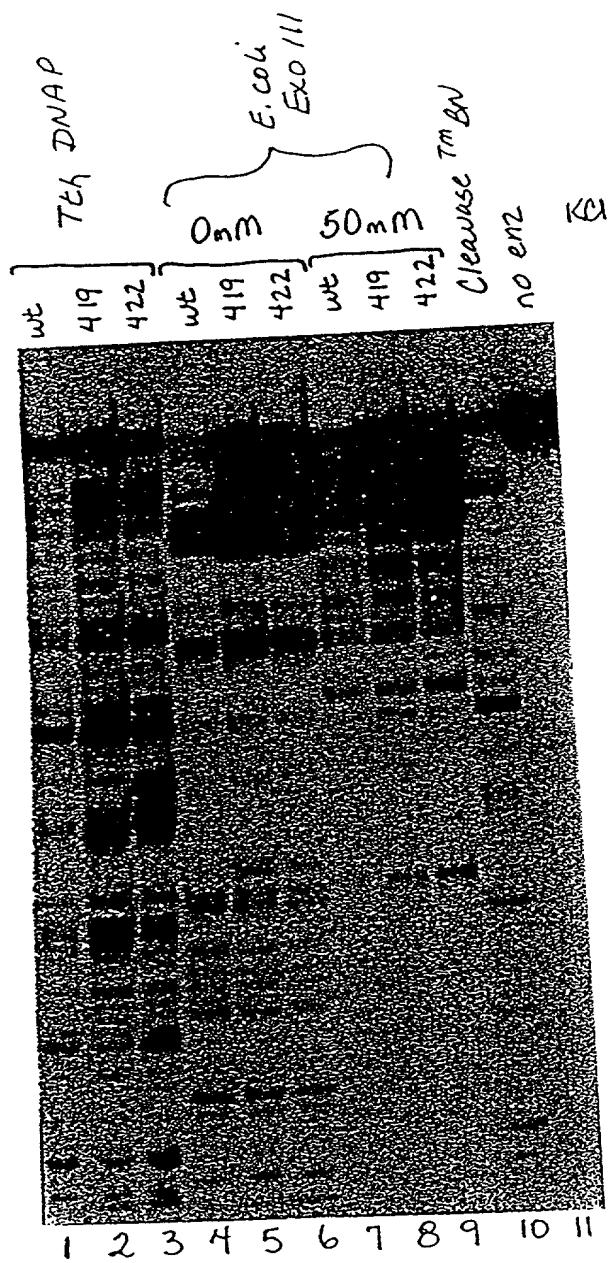


FIGURE 71

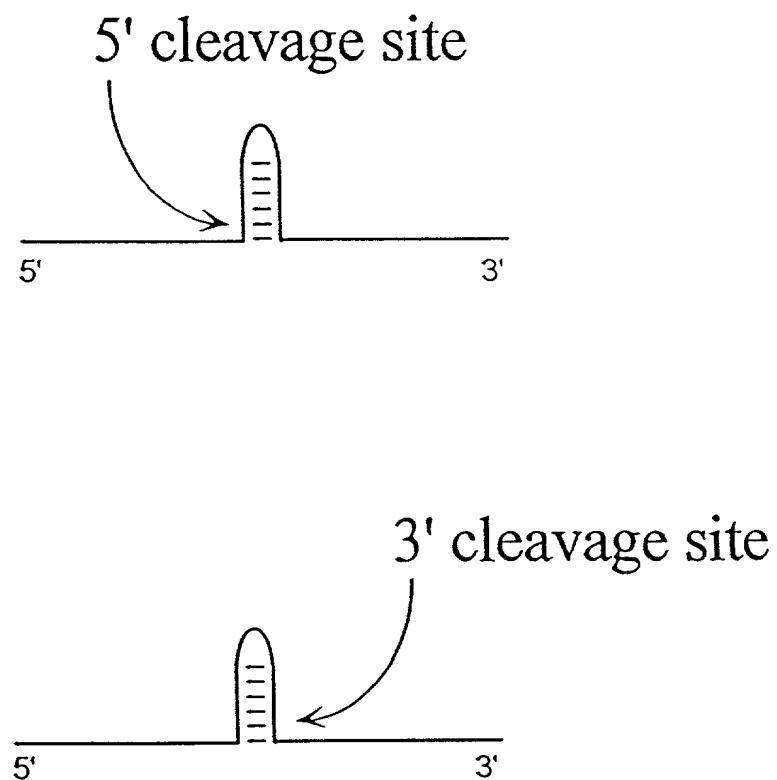


FIGURE 72

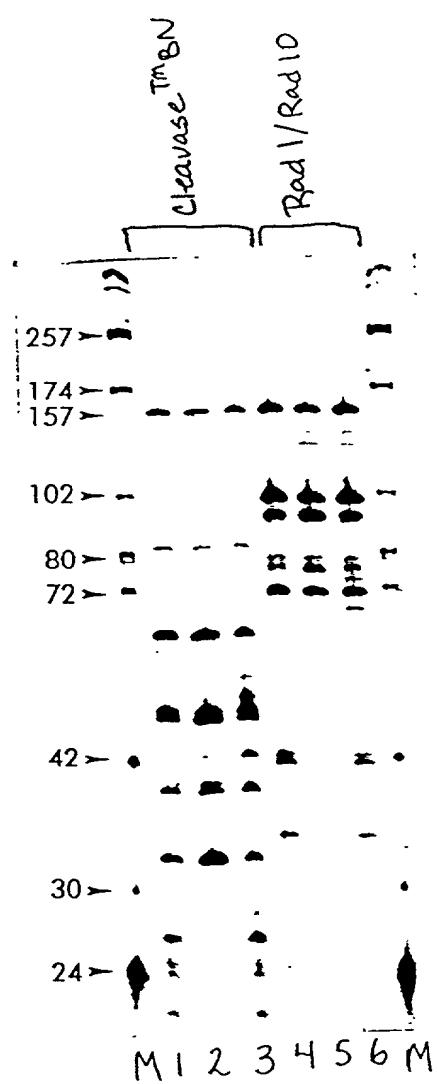
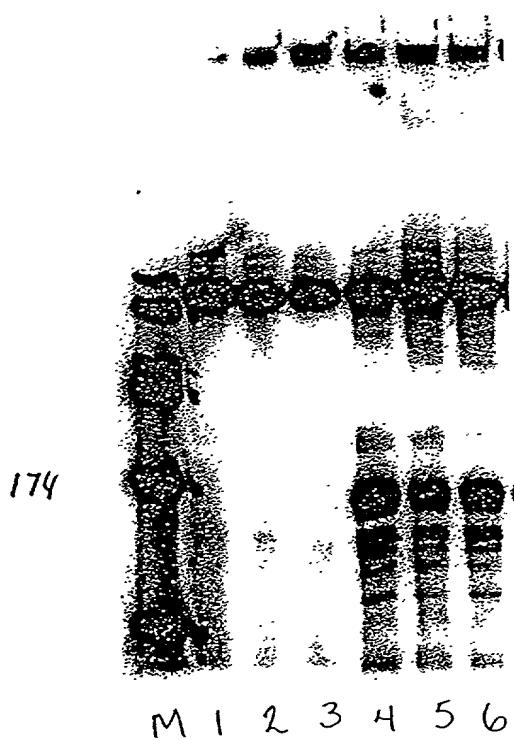


FIGURE 73

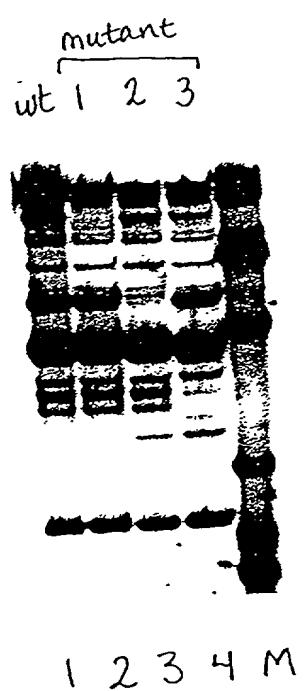
174 175 176 177 178 179



86

FIGURE 74

A



B

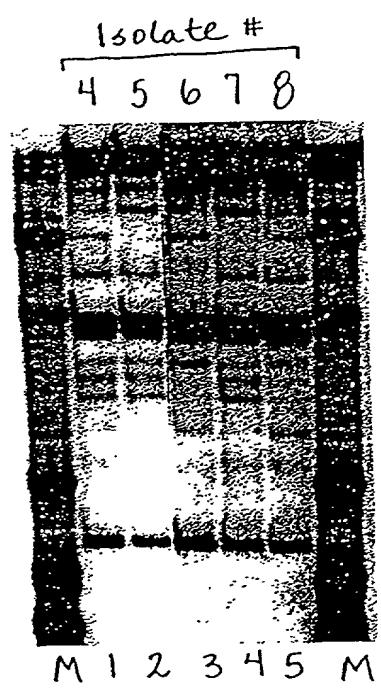
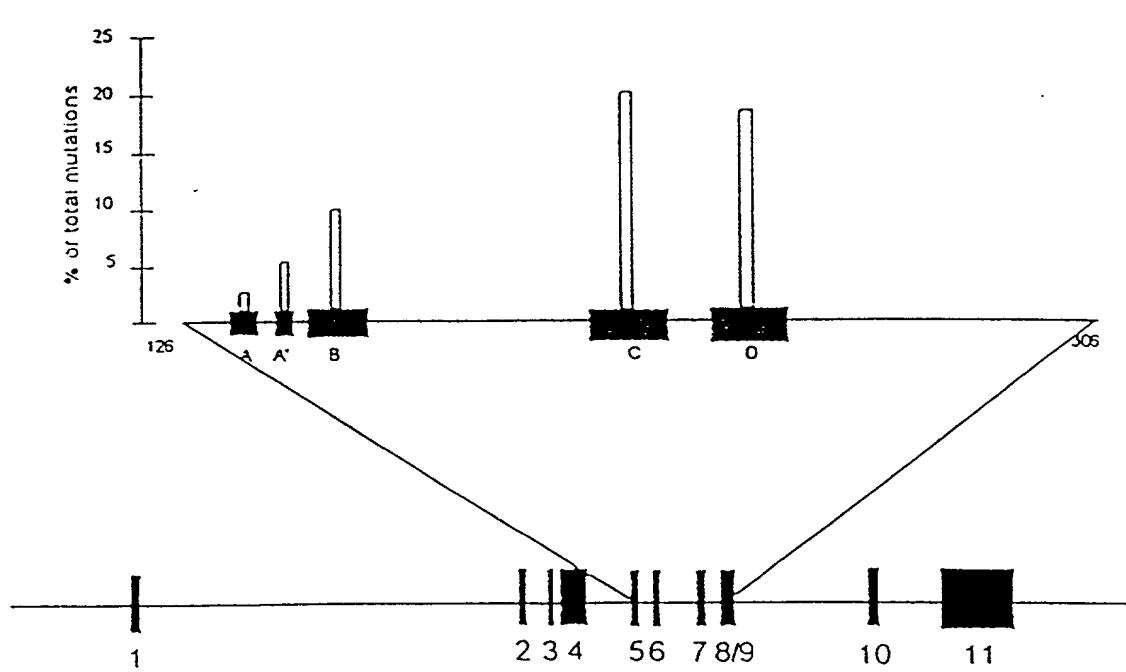


FIGURE 75



FIGURE 76



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FIGURE 77

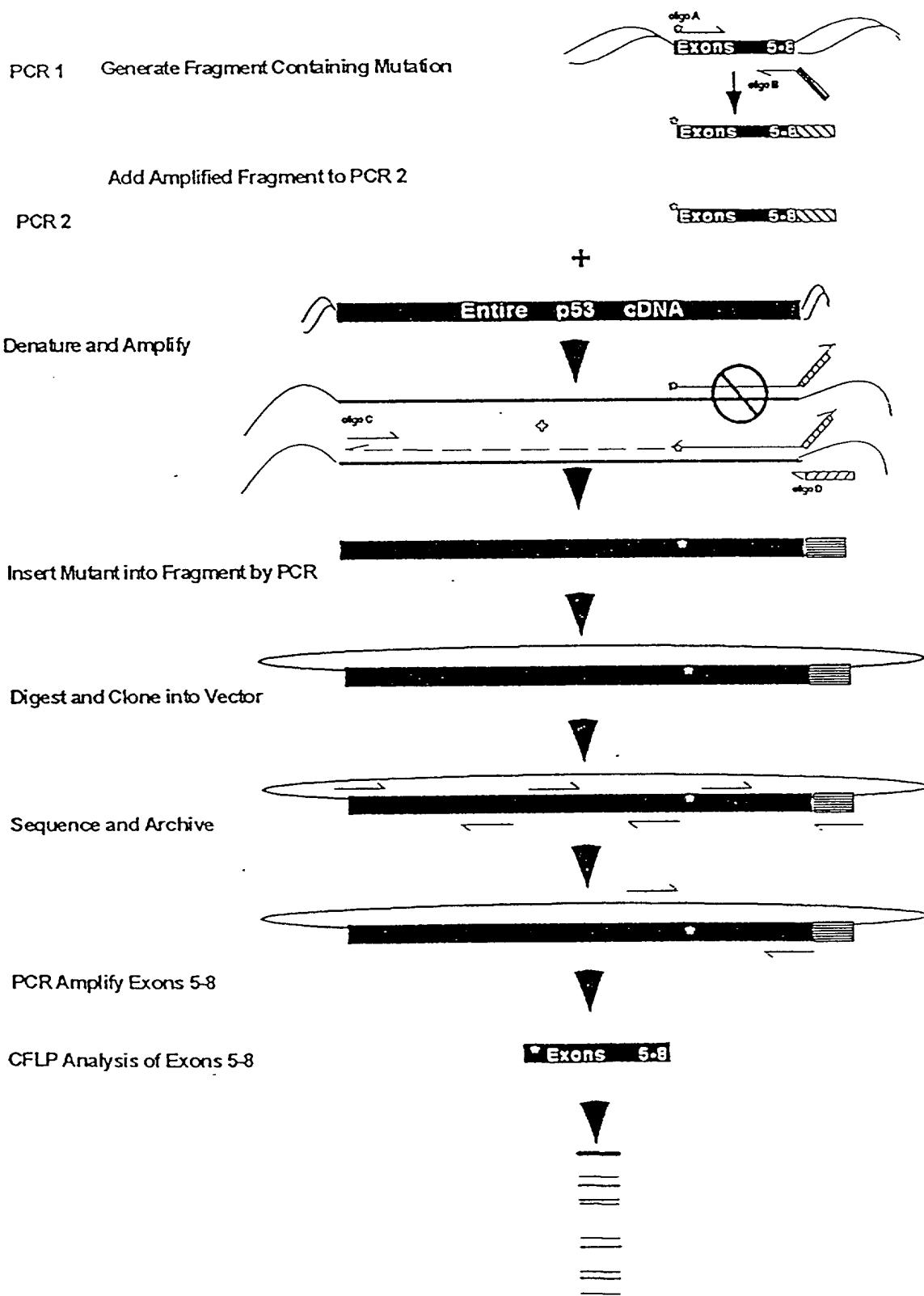


FIGURE 78

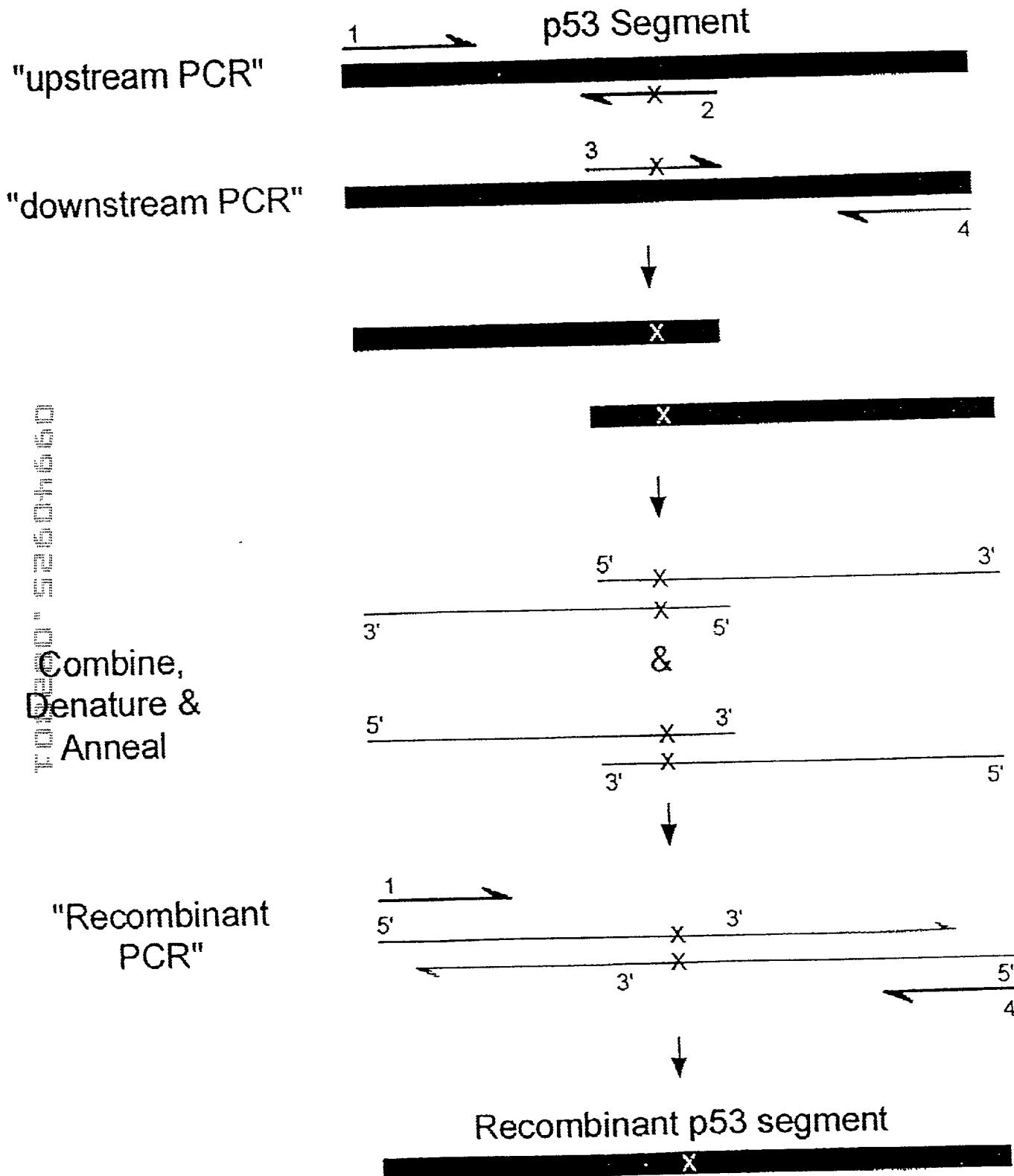


FIGURE 79

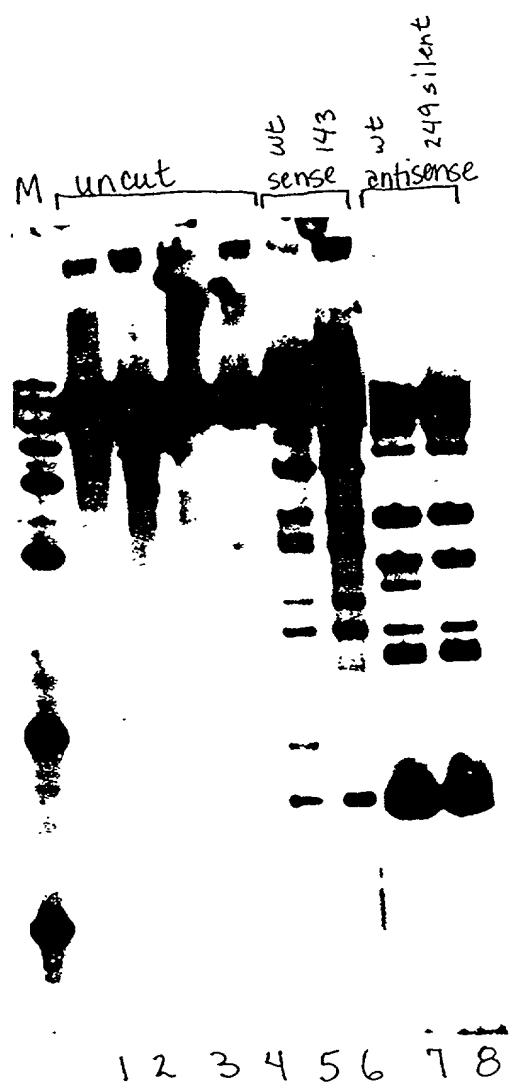


FIGURE 80

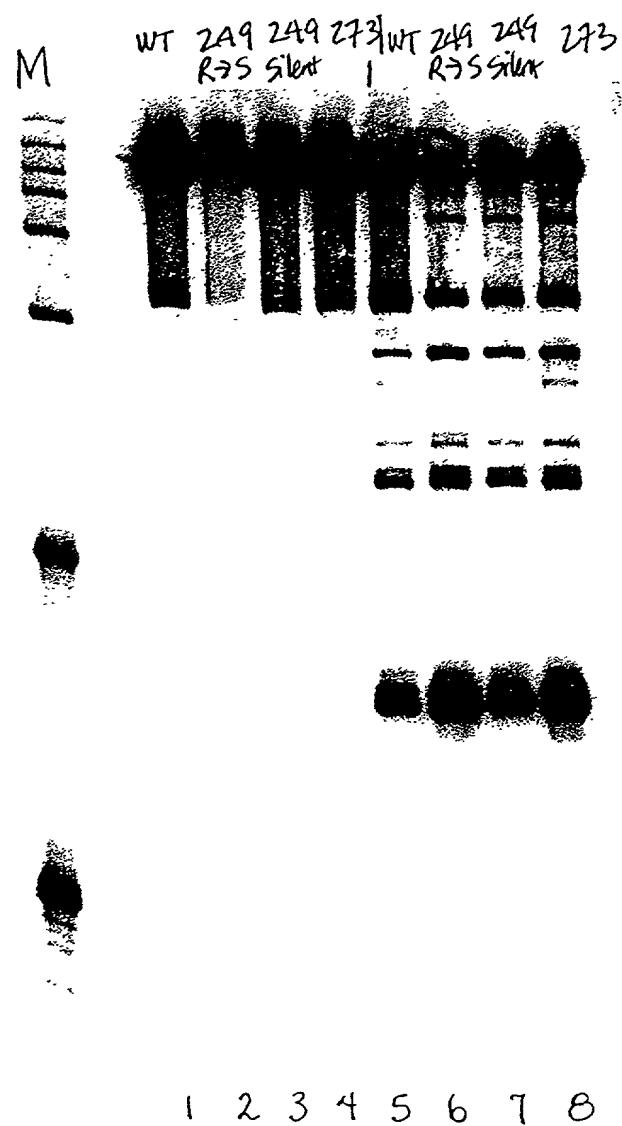
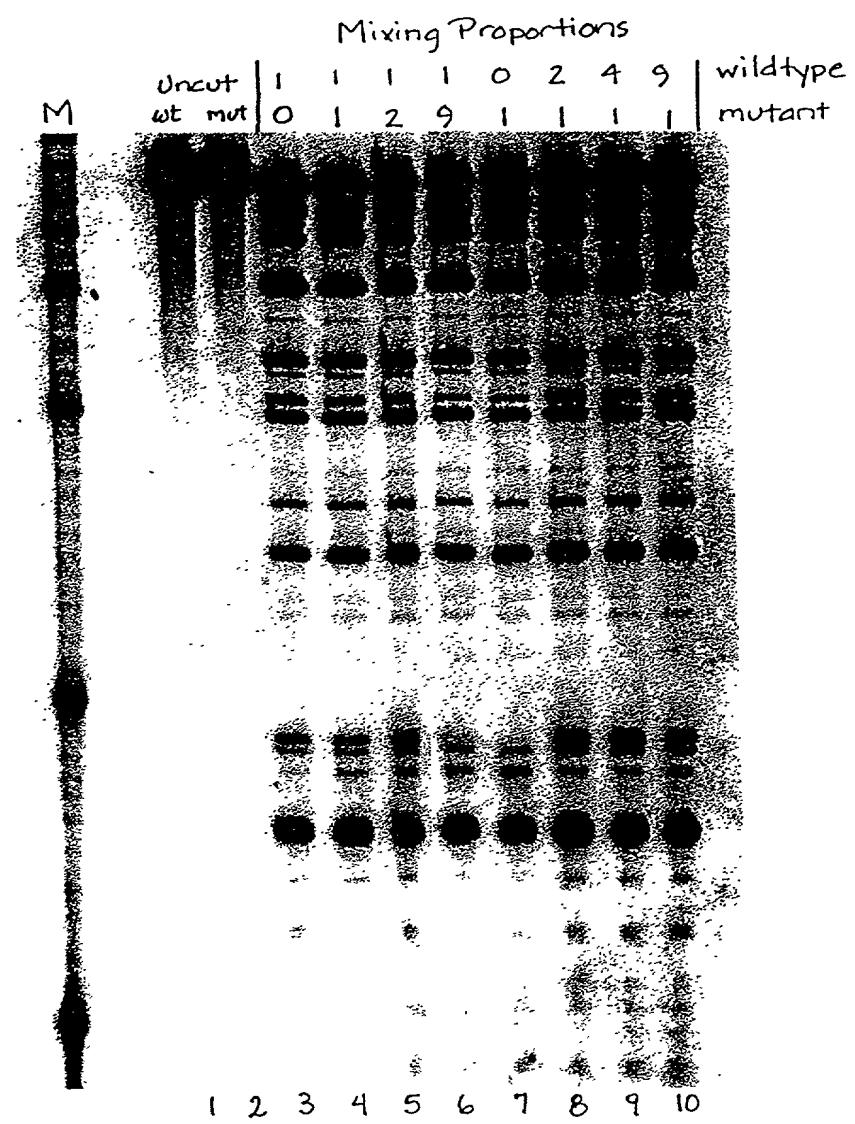


FIGURE 81



44

FIGURE 82

HCV1 . 1 (SEQ ID NO : 121)	1	CTGCTTCA C GCAGAAAGGG CTGCTTCA C GAGAAAGGG CTGCTTCA C GAGAAAGGG CTGCTTCA C GAGAAAGGG CTGCTTCA C GAGAAAGGG CTGCTTCA C GAGAAAGGG CTGCTTCA C GAGAAAGGG	TCTGCCATG TCTGCCATG TCTGCCATG TCTGCCATG TCTGCCATG TCTGCCATG TCTGCCATG	GCGTTAGTAT GCGTTAGTAT GCGTTAGTAT GCGTTAGTAT GCGTTAGTAT GCGTTAGTAT GCGTTAGTAT	GAGTGTCTGTG GAGTGTCTGTG GAGTGTCTGTG GAGTGTCTGTG GAGTGTCTGTG GAGTGTCTGTG GAGTGTCTGTG	50
HCV2 . 1 (SEQ ID NO : 122)						
HCV3 . 1 (SEQ ID NO : 123)						
HCV4 . 2 (SEQ ID NO : 124)						
HCV6 . 1 (SEQ ID NO : 125)						
HCV7 . 1 (SEQ ID NO : 126)						
HCV1 . 1	51	CAGCCTCCAG GACCCCCCT CAGCCTCCAG GACCCCCCT CAGCCTCCAG G <u>T</u> CCCCCT CAGCCTCCAG GACCCCCCT CAGCCTCCAG GCCCCCCCCT CAGCCTCCAG GACCCCCCT	CCCGGGAGAG CCCGGGAGAG CCCGGGAGAG CCCGGGAGAG CCCGGGAGAG CCCGGGAGAG	CCATAGTGGT CCATAGTGGT CCATAGTGGT CCATAGTGGT CCATAGTGGT CCATAGTGGT	CTGCGGAACC CTGCGGAACC CTGCGGAACC CTGCGGAACC CTGCGGAACC CTGCGGAACC	100
HCV2 . 1						
HCV3 . 1						
HCV4 . 2						
HCV6 . 1						
HCV7 . 1						
HCV1 . 1	101	GGTGAGTACA CCGGAATTGC GGTGAGTACA CCGGAATTGC GGTGAGTACA CCGGAATTGC GGTGAGTACA CCGGAATTGC GGTGAGTACA CCGGAATTGC GGTGAGTACA CCGGAATTGC	CAGGACGACC CAGGACGACC CAGGACGACC CAGGACGACC CAGGACGACC CAGGACGACC	GGGTCTTTTC GGGTCTTTTC GGGTCTTTTC GGGTCTTTTC GGGTCTTTTC GGGTCTTTTC	TGGAT-AAA TGGAT-CAA TGGAT-CAA TGGAT-GTAA TGGAT-AAA TGGAT-CAA	150
HCV2 . 1						
HCV3 . 1						
HCV4 . 2						
HCV6 . 1						
HCV7 . 1						
HCV1 . 1	151	CCCGCTCAAT GCCTGGAGAT CCCGCTCAAT GCCTGGAGAT CCCGCTCAAT GCCTGGAGAT CCCACTCTAT GCC <u>GGCC</u> AT CCCGCTCAAT ACC <u>GGAA</u> AT	TTGGGCGGTGC TTGGGCGGTGC TTGGGCGGTGC TTGGGCGGTGC TTGGGCGGTGC	CCCCGCAAGA CCCCGCAAGA CCCCGCAAGA CCCCGCAAGA CCCCGCAAGA	CTGCTAGCCG CTGCTAGCCG CTGCTAGCCG CTGCTAGCCG CTGCTAGCCG	200
HCV2 . 1						
HCV3 . 1						
HCV4 . 2						
HCV6 . 1						
HCV7 . 1						
HCV1 . 1	201	AGTAGTGTG GGTGGAGAA AGTAGTGTG GGTGGAGAA AGTAGTGTG GGTGGAGAA AGTAG <u>GG</u> TTG AGTAGTGTG GGT <u>GG</u> AGAA	GGCCTTGTGG GGCCTTGTGG GGCCTTGTGG GGCCTTGTGG GGCCTTGTGG	TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA	TAGGGTGCCT TAGGGTGCCT TAGGGTGCCT TAGGGTGCCT TAGGGTGCCT	250
HCV2 . 1						
HCV3 . 1						
HCV4 . 2						
HCV6 . 1						
HCV7 . 1						
HCV1 . 1	251	GGGAGTGCC GGGAGTGCC GGGAGTGCC GGGAGT <u>AC</u> GGGAGTGCC	CGGGAGGTCT CGGGAGGTCT CGGGAGGTCT CGGGAGGTCT CGGGAGGTCT	CGTAGACCGT CGTAGACCGT CGTAGACCGT CGTAGACCGT CGTAGACCGT	GC 282	
HCV2 . 1						
HCV3 . 1						
HCV4 . 2						
HCV6 . 1						
HCV7 . 1						

95

FIGURE 83

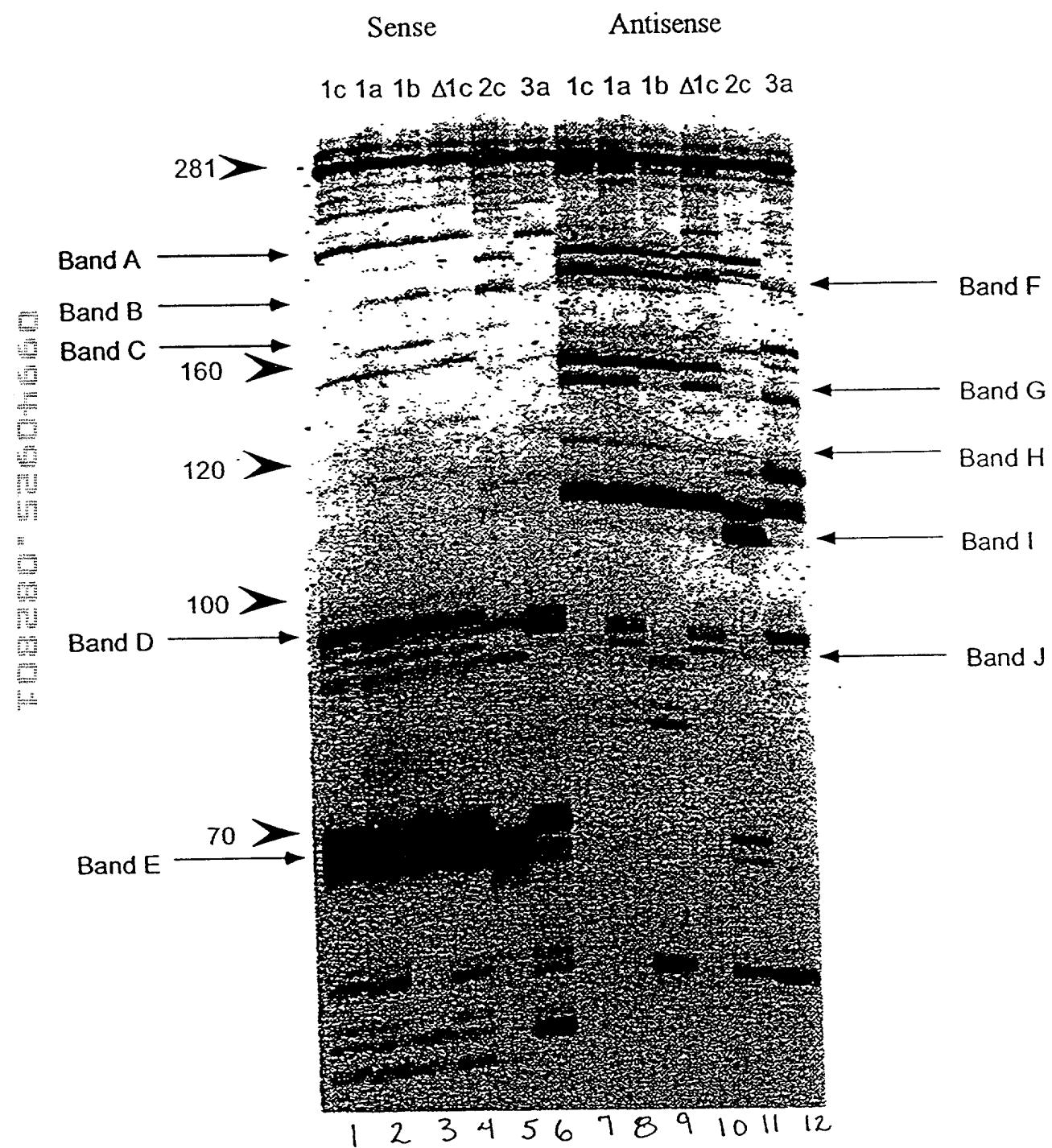


FIGURE 84

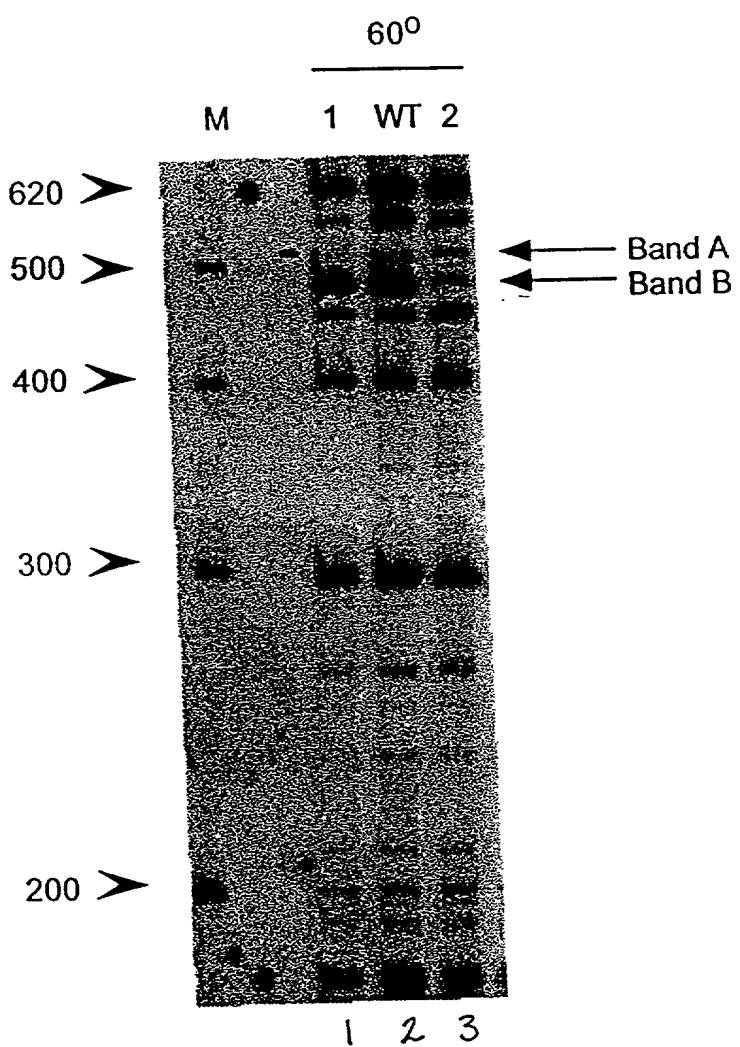


FIGURE 85

98

A. TTP dUTP B. TTP dUTP

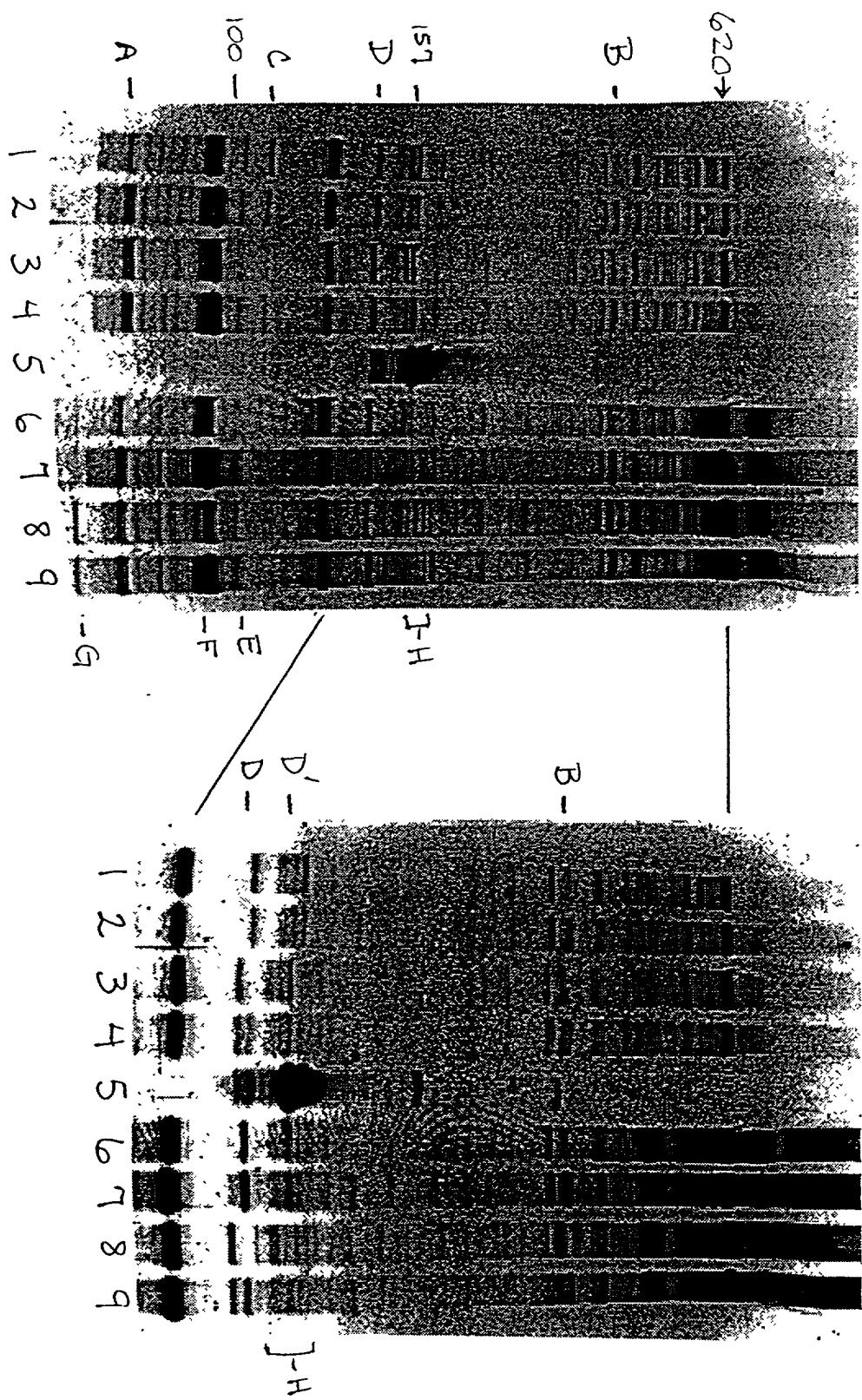


FIGURE 86

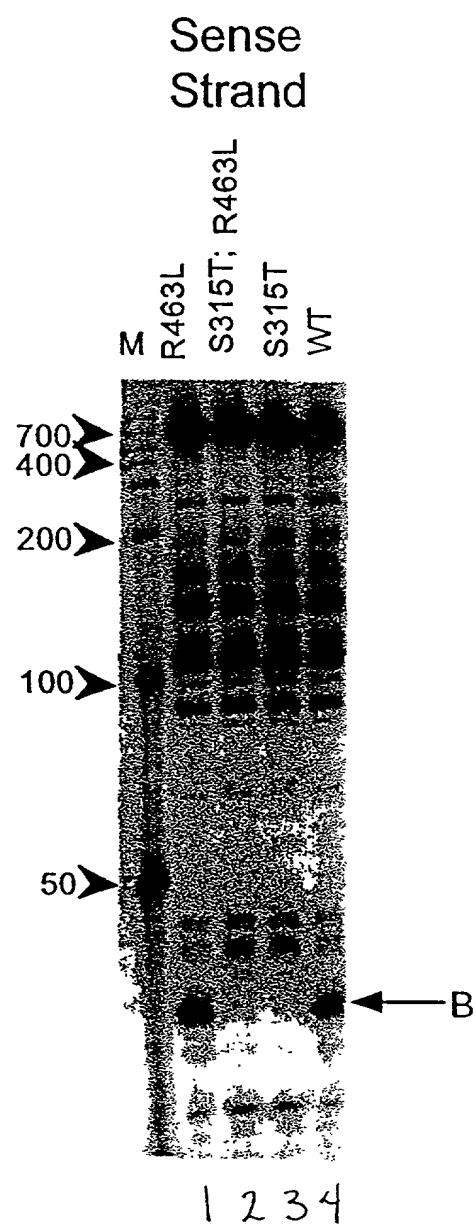
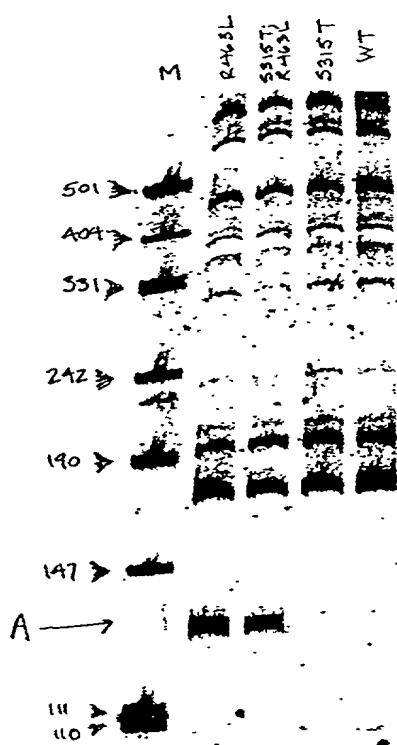


FIGURE 87

Antisense
Strand



1 2 3 4

100

FIGURE 88

Sheet 1/2

10	20	30	40	50	60	
AGA GTTTGATCCT GGCTCAG						1638
AAATTGAAGA GTTTGATCAT <u>GGCTCAGATT</u> GAACGCTGGC GGCAGGCCTA ACACATGCAA TTTAACCTCT CAAACTAGTA CCGAGTCTAA CTTGCGACCG CGTCCGGAT TGTGTACGTT						
70	80	90	100	110	120	
GGCGGAC GGGTGAGTAA						ER10
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA CAGCTGCCA TTGTCCTTCT TCGAACGAAG AAACGACTGC TCACCGCCTG CCCACTCATT						
130	140	150	160	170	180	
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT ACAGACCCTT TGACGGACTA CCTCCCCCTA TTGATGACCT TTGCCATCGA TTATGGCGTA						
190	200	210	220	230	240	
AACGTCGCAA GACCAAAGAG GGGCACCTTC GGGCCTCTTG CCATCGGATG TGCCCAAGATG TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG CCCGGAGAAC GGTAGCCTAC ACGGGTCTAC						
250	260	270	280	290	300	
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGGCAC GATCCCTAGC TGGTCTGAGA CCTAATCGAT CATCCACCCC ATTGCCGAGT GGATCCGCTG CTAGGGATCG ACCAGACTCT						
310	320	330	340	350	360	
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG CCTACTGGTC GGTGTGACCT TGACTCTGTG CCAGGTCTGA GGATGCCCTC CGTCGTCAACC TGA GGATGCCCTC CGTCGTCA						1659
370	380	390	400	410	420	
GGAAATATTGC ACAATGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT CCTTATAACG TGTACCCCGC GTTCGGACTA CGTCGGTACG GCGCACATAC TTCTTCCGGA						
430	440	450	460	470	480	
TCGGGTGTAA AAGTACTTTG AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT AGCCCAACAT TTCATGAAAG TCGCCCCCTCC TTCCCTCATT TCAATTATGG AAACGAGTAA						
490	500	510	520	530	540	
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG CTGCAATGGG CGTCTTCTTC GTGGCCGATT GAGGCACGGT CGTCGGCGCC ATTATGCCTC						
550	560	570	580	590	600	
GGTGCAAGCG TTAATCGGAA TTACTGGCG TAAAGCCAC GCAGGCGGT TGTTAAGTCA CCACGTTCGC AATTAGCCTT AATGACCCGC ATTCGCGTG CGTCCGCCAA ACAATTCACT						
610	620	630	640	650	660	
GATGTGAAAT CCCCCGGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC CTACACTTTA GGGGCCCCGAG TTGGACCCCTT GACGTAGACT ATGACCGTTC GAACTCAGAG						
670	680	690	700	710	720	
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC CATCTCCCCC CATCTTAAGG TCCACATCGC CACTTACGC ATCTCTAGAC CTCCTTATGG						
730	740	750	760	770	780	
GGTGGCGAAG CGGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA CCACCGCTTC CGCCGGGGGA CCTGCTTCTG ACTGCGAGTC CACGCTTCTCG CACCCCTCGT						

101

FIGURE 88

Sheet 1

790 800 810 820 830 840
 AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC
 TTGTCCATAAT CTATGGGACC ATCAGGTGCG GCATTGCTA CAGCTGAACC TCCAACACCGG
 850 860 870 880 890 900
 CTTGAGGCCTT GGCTTCCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA
 GAACCTCCGCA CCGAAGGCCT CGATTGCGCA ATTCAAGCTGG CGGACCCCTC ATGCCGGCGT
 910 920 930 940 950 960
 AGGTTAAAAC TCAAATGAAT TGACGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT
 TCCAATTTTG AGTTTACTTA ACTGCCCGG GGCCTGTTCG CCACCTCGTA CACCAAATTA
 970 980 990 1000 1010 1020
 TCGATGCAAC GCGAAGAACCC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG
 AGCTACGTTG CGCTTCTTGG AATGGACCAAG AACTGTAGGT GCCTTCAGGAA GTCTCTACTC
 1030 1040 1050 1060 1070 1080
 AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTGTCAGCT CGTGTGTGA
 TTACACGGAA GCCCTTGGCA CTCTGTCCAC GACGTACCGA CAGCAGTCGA GCACAAACACT
 1090 1100 1110 1120 1130 1140
 GC AACGAGCGCA ACCC
 AATGTTGGGT TAAGTCCCAC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGG
 TTACAACCCA ATTCAAGGGCG TTGCTCGCGT TGGGAATAGG AAACAACGGT CGCCAGGCC
 1150 1160 1170 1180 1190 1200
 ATG ACGTCAAGTC
 ATG ACGTCAAGTC
 CGGGAACTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC
 GCCCTTGAGT TTCCCTCTGAC GGTCACTATT TGACCTCCCT CCACCCCTAC TGCAGTCAC
 1210 1220 1230 1240 1250 1260
 ATCATGGCCC TTA
 ATCATGGCCC TTACGA
 ATCATGGCCC TTACGACCAAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAACCG
 TAGTACCGGG AATGCTGGTC CCGATGTGTG CACGATGTTA CCGCGTATGT TTCTCTTCG
 1270 1280 1290 1300 1310 1320
 ACCTCGCGAG AGCAAGCGGA CCTCATAAAAG TGCGTCGTAG TCCGGATTGG AGTCTGCAA
 TGGAGCGCTC TCGTTCGCCT GGAGTATTTC ACGCAGCATC AGGCCTAACCC TCAGACGTT
 1330 1340 1350 1360 1370 1380
 TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACCG GTGAATACG
 AGCTGAGGTA CTTCAAGCCTT AGCGATCATT AGCACCTAGT CTTACGGTGC CACTTATGCG
 GC CACTTATGCG
 1390 1400 1410 1420 1430 1440
 TCCCCGGGCCT TGTACACACCC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAAGTAGG
 AGGGCCCGGA ACATGTGTGG CGGGCAGTGT GGTACCCCTCA CCCAACGTTT TCTTCATCC
 AGGGCCCGGA ACATG
 1450 1460 1470 1480 1490 1500
 AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT GAAGTCGTA
 TCGAATTGGA AGCCCTCCCG CGAATGGTGA AACACTAAGT ACTGACCCCA CTTCAAGCAT
 1510 1520 1530 1540 1550
 CAAGGTTAACCC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA.....
 GTTCCATTGG CATCCCCCTG GACGCCAACCG TAGTGGAGGA AT.....

1638 (SEQ_ID NO:151)
*E. coli*rrSE (SEQ_ID NO:158) 0 . AAATTGAAAGAGTTGATCATGGCTCAGATTGAACGCTGGGGCAAGGCCTAACACATGCA
Cam. jejuns (SEQ_ID NO:159) 0 . TTTTATGGAGAGTTGATCCTGGCTCAGAGTGAACGCTGGGGCGTGCCTAACATGCA
Stp. aureus (SEQ_ID NO:160) 0 . TTTTATGGAGAGTTGATCCTGGCTCAGGATGAACGCTGGGGCGTGCCTAACATGCA

AGAGTTTGATCCTGGCTCAG
 GCGGACGGG

ER10 (SEQ_ID NO:152)
*E. coli*rrSE
Cam. jejuns
Stp. aureus

60 AGTCGAAACGGTAACAG--GAAGAAGCTTGCTTCCTT-
 62 AGTCGAACGAT-GAAGCTTCAAGCTGCTAGAAGTGGAT-
 61 AGTCGAGCAA-CGGACGAGAAAGCTTGCTCTGATG-
 TGACTAA
 114 TGAGTAATGTCGGAA-AACTGCCTGATGGAGGGATAACTACTGGAACGGTAGCTAAATA
 114 TGAGTAAGGTATAGTTAATCTGCCCTAACAGGACAAACAGTTGAAACGACTGCTAAATA
 113 TGAGTAACACGGATAACCTACCTAACATAAGACTGGATAACTTGGGATAACTCGGGAAAACGGAGCTAAATA

CCGCATAAC-GTCGCAAGAC-
 175 CTCATAACTCTGCTTAACACAAGTTGAGTAGG-GAAAG-
 176 CGCGATAATTGTTGAACCGCATGGTCAAAAGTGAAGACGGT-
 175 CCCGATAATTGTTGAACCGCATGGTCAAAAGTGAAGACGGT-

CCATCGGATGTCGGCCAGATGGGATTAGCTAGTAGGTGGGTAACGGCTCACCTAGGGCAGCA
 221 GTGTTAGGATGAGACTATAGTATAGCTAGCTAGTTGGTAAGGTAACTGGCTTACCAAGGCAACGA
 221 CGCTTAACCTGGCTGCATAGCTAGTTGGTAAGGTAAACGGCTTACCAAGGCAACGA
 229 CTTATAGATGGATCCGGCTGCATTAGCTAGTTGGTAAGGTAAACGGCTTACCAAGGCAACGA

TCCCTAGCTGGTCTGAGAGGATGCCAGCAACTGGAAACTGAGAACCGGTCCAGACTCCTA
 283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCAGTCAGTCAACTGGAAACTGAGAACCGGTCCAGACTCCTA
 283 TAGTGGCCGACCTGAGGGTGTATGGCCACACTGGAAACTGAGAACCGGTCCAGACTCCTA
 291 ACTCTTA

CCGGAGGCAGCAGTGGGAAATTGGCACAAATGGGGCAAGCCATGCAAGCTGAGCCATGCCATGCCATGCC
 345 CGGGAGGCAGCAGTGGGAAATTGGCAATGGGGAAACCGCTGAGCCAGCAACGGCTGAGCCATGCCATGCC
 345 CGGGAGGCAGCAGTGGGAAATTGGCAATGGGGAAACCGCTGAGCCAGCAACGGCTGAGCCATGCCATGCC
 353 CGGGAGGCAGCAGTGGGAAATTGGCAATGGGGAAACCGCTGAGCCAGCAACGGCTGAGCCATGCCATGCC
 353 CGGGAGGCAGCAG

TATGAAGAAGGCCCTCGGGTTGTAAGTACTTCAGCGGGGAGGA-GGGAGTTAAAGTTAAT
 407 GAGGTGACACTTTGGAGGGTAACCTCTTCTTGGGAAG-
 407 AGTGTGATGAGGTCTTGGATGATGTAACATCTGTTATTAGGGAAAGAACATATGTTAAGTAAAC

ACCTTTGCTCATTGACGTTACCCGGCAAGAACGCCAGCCGTAACCTCCGTGCCAGGCC
 455 C-TGACGGTACCTAACGGATAAGCACCCTGCTAACCTCCGTGCCAGGCC
 415 AGTGTGACATCTTGGACGGTACCTAACGGTAACCTAACGGCAAGGCCAGGCC

E. coli rrSE
Cam. jejuns
Stp. aureus

1659 (COMPL)

E. coli rrSE
Cam. jejuns
Stp. aureus

1659 (COMPL)

1001

FIGURE 89

Sheet 3/3

105'

SB-3	(SEQ ID NO:157)
SB-4	(SEQ ID NO:154)
E.colirrSE	1142 GGGACTCAAAGGAGACTGCCAGTGTAACTGGAGGAAGGTGGGATGAGCTCAAGTCATCC
Cam.Jejuns	1122 GAGCACTCTAATAAGTAGCTGCCTCG-TAAGGAGGAGGAAGGTGGACGAGCTCAAGTCATCC
	1122 GAGCACTCTAATAAGTAGCTGCCTCG-TAAGGAGGAGGAAGGTGGGATGACGCTCAAATCATCC

၁၃

SB-3			
		ATGGGCCTTACGA	
SB-4			
		ATGGCCCTTACGACCGGCTACACAGTGCTACAATGGCCATACAGAGAGCGACCTCC	
E.colirrse	1204	ATGGCCCTTACGACCGGCTACACAGTGCTACAATGGCCATACAGAGAGCGACCTCC	
Cam.jejun5	1183	ATGGGCCTTATGCCAGGGGACACACGTGCTACATGGCATATGAAATGAGAACGCGATAACCC	
Stp.aureus	1214	ATGCCCTTATGATTGGCTACACAGTGCTACAATGGACAATAACAAAGGCAGCGAAACCC	

E.colirrse	1266	GCGAGGCAAGGGACCTCATAAAGTGCGTCGGATGGTGCACCTGGAC
Cam.jejuns	1245	GCGAGGTGGAG=CAAATCTATAAAATATGTCGCCAGTCGAATGTTCTGCAACTCGAGGAG
Stp.aureus	1276	GCGGGTCAAGCAAATCCATAAAGTTGTTCTCAGTTGGATGTTGACTCGACTTA
E.colirrse	1328	CATGAAGTCGGATCGCTAGTAATCGTGGATCAGA=ATGCCACGGTAATACGTTCCGGG
Cam.jejuns	1306	CATGAAAGCCGGAAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTAATACGTTCCGGG
Stp.aureus	1338	CATGAAAGCTGGAAATCGCTAGTAATCGTAGATCAGC=ATGCTACGGTAATACGTTCCGGG
1743 (compl)		CGGTAATACGTTCCGGG

E.colirrSE	1389	CTTGACACACCCCCGTCAACCATGGAGTGGTTGCAAAGAAGTAGGTAGCTAACCT
Cam.jejun5	1368	CTTGACTCACCGCCCGTCAACCATGGAGTTGAACTCGAAGCCGGAACT-T-A-A-
Stp.aureus	1399	ATGTACACACACGGCCGTCAACCACGGAGCTTGAACACCGAAGCCGGTGGAGTAACCT
1743 (compl.)		CTTGAC

E.colirrse 1451 TCG_GAGGGCGCTTACCACTTGTGATTAAGCTGGG
 Cam.jejuns 1427 AC---T-AGTTACCGTCCACAGCTGGGATCAGCGACTGGGTAACAGGTAACCC
 Stp.aureus 1461 TTAGGAGCTAGCGTCGAAGGTGGACAAATGATTGGGTGAGTCGTAACAAGGTAGCCG

E.colirrse	1512	TAGGGAACTTGGGTTGGATCACCTCTTA-----
Cam.Jejun	1485	TAGGGAAACCTGGGTTGGATCACCTCTT-----
Stp.aureus	1523	TATCGGAAGGTGGGCTGGATCACCTCTTCT

FIGURE 90

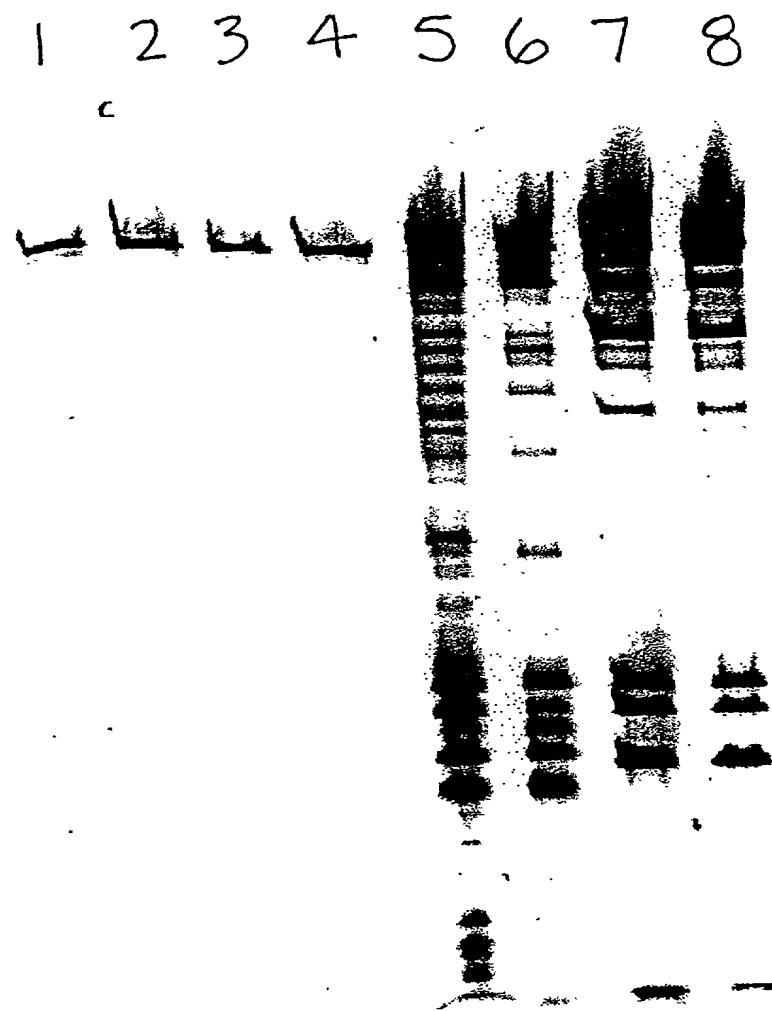
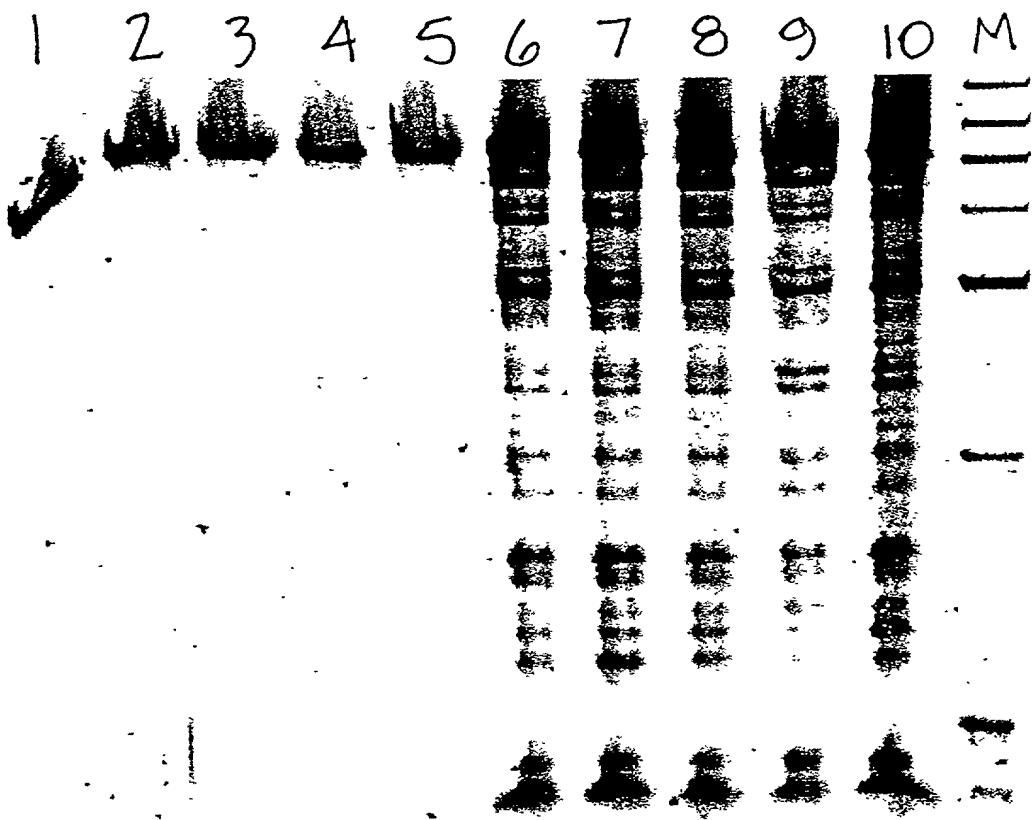


FIGURE 91

A.



B.

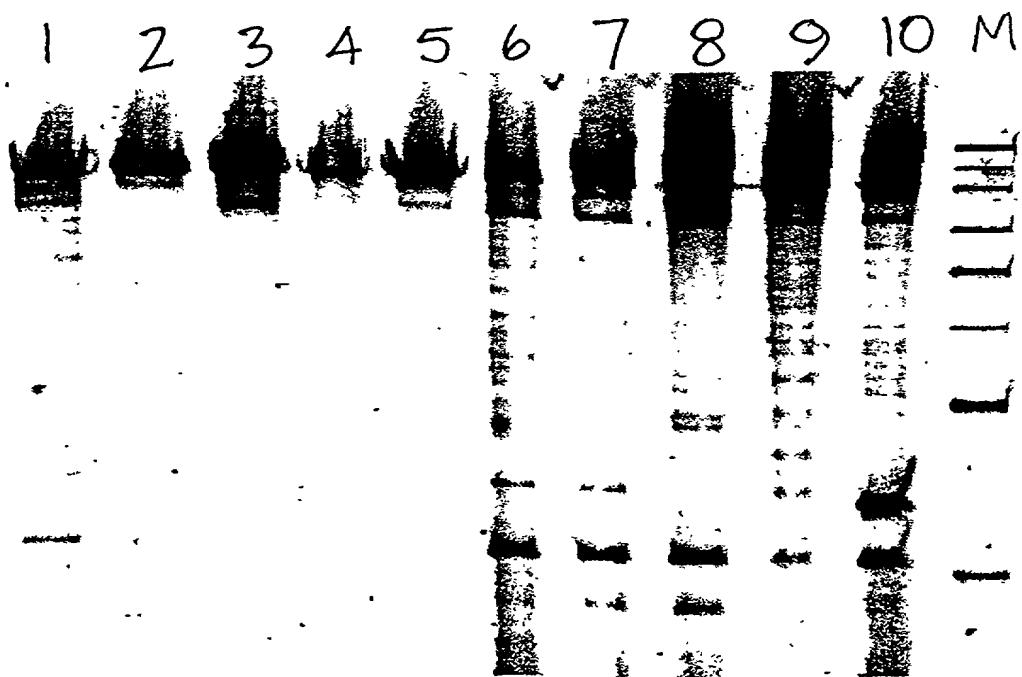


FIGURE 92



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FIGURE 93

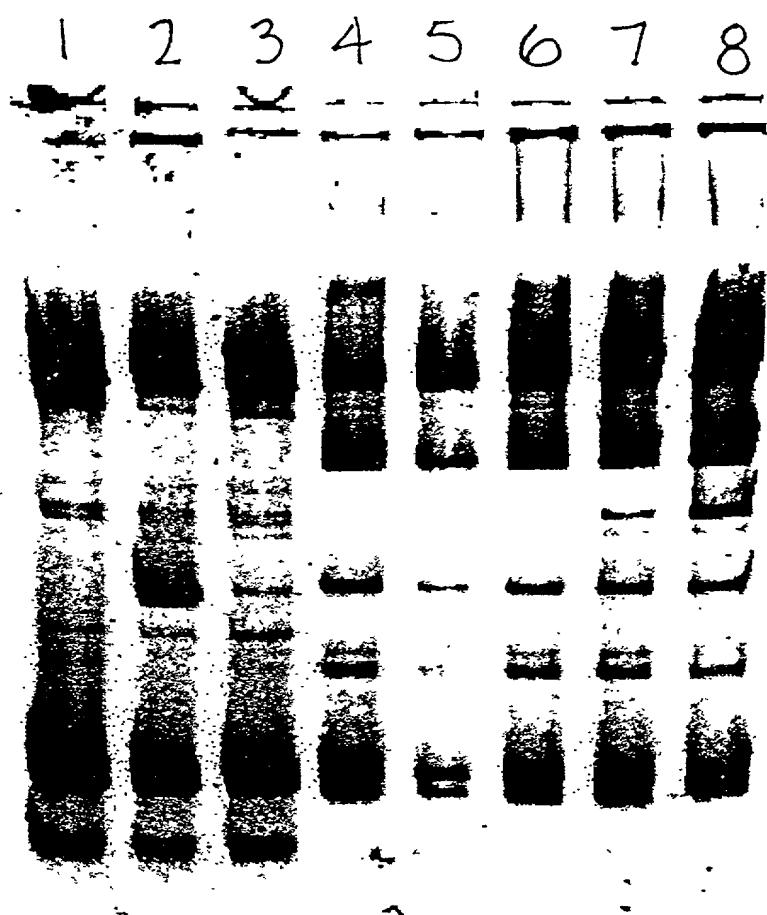


FIGURE 94

